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Regult
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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10731.394 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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CC871613 NDL 2,2A24
DN468758 USDA-FP 1
BZ569544 msh2 105.
CB065364 EST645045
CL678544 PRIO123b
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AG841316 CVyza asc
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ALIGNMENTS

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	57.2%; Score 820; DB 10; Length 820;	Query Match Rest Local Similarity	Query
			ORIGIN
	note="Vector: pEpifos-5 Fosmid vector"		200
	California"	var.	
.•	ob xref="taxon:54126"	/db	
	strain="California"	/st	
	organism="Fiscionends pacificus"	/mo	
		source 1.	80
٠	Location/Qualifiers		FEATURES
	fosmid ends.	Class: fosmi	
	177	Seq primer:	
	couver, Canada.	sequenced at	
	was generated at Caltech, Pasadena, USA and end	This library was	
	Rmail: raif commerciationingen mng de	Email: ralf	
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			COMMENT
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:	REB. 34 (1), D441-D444 (4004)		OURNAL
	pacificus		
٠.	AppaDB: an AcedB database for the nematode satellite organism		TITLE
	Kahlow, U., Geisler, R. and	-	AUTHORS
,		••	REFERENCE
	erazoa, memacoua, curomacorea, orprogasterraa, eridae, Pristionchus.	Neodiplogasteridae;	
٠.	matoda. Chuamadayaa.		ORGANISM
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pacificus var.
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         Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 895)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisle
                                                                                     survey sequence.
CL665529
CL665529.1 GI:5
                                                                Pristionchus pacificus
AppaDB:
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Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
CC871613

OBL 2A24.SP6 Notre Dame Liverpool Aedes aegypti genomic NotreDame Liverpool-2A24, genomic survey sequence. CC871613

CC871613.1 GI:33231623
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Max-Planck-Institute for Deve
Spemannatr. 37-39, Tuebingen
Tel: 00497071601371
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Contact: Sommer RJ
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/mol_type="genomic_DNA"
/strain="California"
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j. .895
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Pred. No. 8.7e-130;
0; Mismatches 12;
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Best Local Similarity 70.4
516; Conservative
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Other GSSs: NDL.2A24.T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       κυκαιγοτα; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera, Endopterygota, Diptera; Nematocera; Culicoidea;
Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
1 (bases 1 to 682)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: enta@tigr.org
Library was provided by David
Seq primer: SP6
Class: BAC ends.
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GTGTATGACGTTACCGGTGCGGGCGACACGGTGATTGGCGTCCTGGCGGCAACGCTGGCA
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/clone lib="Notre Dame Liverpool"
/clone lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site 1: Hind III; The library was
prepared from whole body tissue of newly hatched Li larvae
by David Severson at the University of Notre Dame and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
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Pred. No. 1.8e-109;
0; Mismatches 161;
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                                   364 GAAGAAGGTTTCGAAGGTGTTGATCCGCAGCCGCTGCACGAGCGGATTAATCAGGCGCTG
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                                                                                                                                          323,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DN468758 722 bp mRNA linear BST 01
USDA-FP 142740 Diaphorina citri Kuwayama (Hemiptera: Peyll
Diaphorina citri cDNA clone WHDc040_E04 5', mRNA sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001 South Rock Road, Ft. Pierce, F. Tel: (772) 462-5898, (772) 462-5940 Fax: (772) 462-5986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2006)
Contact: Wayne Hunter, Phat Dang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hunter, W.B., Dang, P.M. and McKenzie, C. Gene expression in adult Asian citrus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Neopteara; Paraneoptera; Hemiptera; Sternorrhyncha; Psylloidea; Psylloidea; Psylloidea; Diaphorina.

1 (bases 1 to 722)
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Whunter@ushrl.ars.usda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S. Horticultural Research Lab,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuwayama (Hemiptera: Psylloidea)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer: T3 Primer
                                                                                                                                            Conservative
                                                                                                                                                                                                                          /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; source: Colonies maintained by Dr. McKenzie, USHRL, Fort Pierce, FL. A high quality EST with at least 200 contiguous bases at Trace Tuner score of 20 or better. Library construction by Laura Hunnicutt, USDA, ARS, U.S. Horticultural Res. Lab, Ft.Pierce, FL, USA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Diaphorina citri"
/mol_type="mRNA"
/db_xref="taxon:121845"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       dev_stage="adults"
                                                                                                                                                                                                                                                                                                                                                                                                            sex="Mixed genders"
tissue_type="whole body"
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                                                                                                                                                         Score 323; DB 8; 1
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Spencer,D.H., Raymond,C.K., Smith,E.E.,
Burns,J.L., Kaul,R. and Olsen,M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Washington Box 352145, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whole-Genome-Sequence variation among Psedomonas aeruginosa library J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BZ569854.1 GI:27204915 GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            craymond@u.washington.
                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:287"
/clone="msh2 105"
/clone_11b="msh"
/clone_11b="msh"
/note="Environmental isolate.
library."
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/strain="MSH"
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                                              Email: habn@ccrc.uga.edu
TIGR sequence name: MTMAB49TK
TIGR sequence name: nailable &
Seq primer: SKmod (CTA 9AA CTA
Location/Qualifiers
                                                                                                                                                                                      Unpublished (2001)
Contact: Michael G. Hahn
Complex Carbohydrate Research Center
                                                                                                                                                                                                                                       1 (bases 1 to 682)
Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Var
Utterback,T., Cho,J. and Fraser,C.M.
ESTs from roots of Medicago truncatula treated with
oligogalacturonides of DP 6-20
                                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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EST645045 HOGA Medicago truncatula
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                                                                                                                              Fax: 706-542-4412
                                                                                                                                                        University of Georgia
220 Riverbend Road, A
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/organism="Medicago truncatula"
/mol_type="mRNA"
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  CCCGAGGACACCCC
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/Clone libe-"ROGA"
/Clone libe-"ROGA"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/ROGI; cDNA was prepared from polyA+ enriched RNA. The cDNA
XNOI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in SOLR cells."
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/db_xref="texon:3880"
/db_xref="texon:3880"
/clone="HCAR-211"
/tissue_type="3 day old seedling roots"
/dev_stage="24 hours after treatment in the dark at with 0.5 mg/ml oligogalacturonides (DP 6-20) in the presence of 100 ug/ml Gentamicin"
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RESULT 7 CL678544/c

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                                                pacs2-164_4762.y2 pacs2-164 Pseudomonas aeruginosa genomic
pacs2-164_4762, genomic survey sequence.
BZ564465
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AppaDB: an AcedB database
Pristionchus pacificus
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Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 593)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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                 BZ564465.1
GSS.
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This library was generated at Caltech,
sequenced at Vancouver, Canada.
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/mol_type="genomic DNA"
/strain="California"
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Pred. No. 4.6e-56;
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Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spencer, D.H., Raymond, C.K., Smith, B.E., Burns, J.L., Kaul, R. and Olsen, M.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: craymon
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Washington Box 352145, Seattle, WA
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                                                                                     TCGAGCTGGAAAATGCTGTACGTGGACGTGCAGATACAGGCTTTGGCGTGATGACCGAAG
                                                                                                                                                                                          TGATTGGCGTCCTGGCGGCAACGCTGGCAGCGGGTAATTCGCTGGAAGAAGCCTGCTTCT
                                                                                                                                                                                                                                                                                                                                               GTAAGACCGAAGAAGAGTTGTTGAGCGCGCATGAAACTGATTGCCGATTACGAACTCT
                                                                                                                                                                                                                                                                                                                                                                          ATCGCGGCGCCAGCCTGATCACCCCGAACCTGTCCGAATTCGAGACCATCGTCCGTT
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             ACCAATTGCTGTTGGCAATCGAAGACGCCCGCGAACACGGGG
                                    AGGAACTGAAGCTGGCCGTAGCGGCAGCGCGTAAACGTGGTG 1018
                                                               CCGAACTGCGTCGCGCGGTGCAGCGCGAGCAGGGTTCCGAGCGTGGCGTGCTGGGCCTGG
                                                                                                                TGGCCAACCTGGCCGCCGGCATCGTGGTCGGCAAGCTGGGTACCGCGGCGATCAGCGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="pacs2-164_4762"
/clone_lib="pacs2-164"
/note="clinical isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Pseudomonas
/mol_type="genomic DNA
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|strain="2-164"
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Pred. No. 1.1e-39;
0; Mismatches 245
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Local Similarity
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Submitted (29-OCT-2004) Takuji Sasaki, National Institute of
Submitted (29-OCT-2004) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki, 305-8602, Japan
(B-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7448]
The orientation of the sequence is from T7 side of the BAC clone.
Location/Qualifiers
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Breeding Science 54, 273-279 (2004)
2 (bases 1 to 879)
Sasaki,T., Matsumoto,T. and Wu,J.
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rcrcceereceeecearaccercarceecacecreecerearecreeeeecreecear
                                                 TTACCGGTGCGGCGACACGCTGATTGGCGTCCTGGCGGCAACGCTGGCAGCGGGTAATT
                                                                                                        TGTACCGCGATGGCGAGGTTAC---GCACTTCCCGACCATGGCGCGCGAGGTGTTCGATG
                                                                                                                                                            TGCTGCAACCGGGTAAAGCGCCGCTGCATATGCCAACCCCAAGCGCAGGAAGTGTATGACG
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/mol type="genomic DNA"
/culTivar="Kasalath"
/db xref="taxon:39946"
/clone="K0061H04_F"
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BZ554342 1195 bp DNA linea pacs1-60_464.sl pacs1-60_Pseudomonas aeruginosa pacs1-60_464, genomic survey sequence.
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Appabb: an Acedb database for the nematode
Pristionchus pactificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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This library was generated at Caltech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Max-Planck-Institute for Developmental Biology Spemannetr. 37-39, Tuebingen D-72076, Germany
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Neodiplogasteridae; Pristionchus.
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                                                                                                                                                          AACATCATCAAGAAGATCCAACAGGATAAAAAAGGCTAA 1434
                                                                                                                                                                                                                                 GTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGACGGTTGCTCGACGACC 139:
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/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Pristionchus pacificus"
|mol_type="genomic DNA"
|strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:54126"
/clone_lib="Mixed stage
/ar. California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            11.1%; Score 159; DB 10; 100.0%; Pred. No. 2.9e-34;
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genomic clone
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RESULT 12
BE332786
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                               BB332786
us53d03.x1
similar to
sequence.
BE332786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
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Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BZ554342
BZ554342.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
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                                                                                                                                                           CCGCGGCGATCAGCGCGCCCGAACTGCGTCGCGCGGTGC 428
                                                                                                                                                                                                                                                                                                                                                                           TIGCCGATTACGAACTCTCGGCTCTGTTAGTGACCCGTTCCGAACAGGGTATGTCGCTGC 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGCTGTTGTCGGTAAATGTAAGACCGAAGAAGATTGTTGAGCGCGCCATGAAACTGA 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTACCGATTTTGAGCGCTACCGCGGCGCTACGCTGTTAACGCCGAATCTCTCGGAATTTG 598
                                                                                                                                                                                            CCTCCACGGTTTCGCCGATCGAGCTGGAAAATGCTGTAC 937
                                                                                                                                                                                                                                  TGCCGTCCGCGGTGGGCCTGGCCAACCTGGCCGCCGGCATCGTGGTCGGCAATCTGGGTA
                                                                                                                                                                                                                                                                 TGGAAGAAGCCTGCTTCTTTGCCAATGCGGCGCTGGCGGCGGGTGGTCGGCAAACTGGGAA
                                                                                                                                                                                                                                                                                                      CCGGTGCTGGCGATACGGTCATCTCCACCCTGGCCGCGGCGCGTTGCCGCCGGCGAGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAGCGAACTCGACCTCGGCGCCTTGCTGGTGACCCGGCGAGCATGGCATGACCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="pacs1-60_464"
/clone lib="pacs1-60"
/note="clinical isolate 1-60
library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
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                           505 bp mRNA linear EST 14-JT Perkins LRH Mus musculus cDNA clone IMAGE:3216101 SW:RFAE_ECOLI P76658 ADP-HEPTOSE SYNTHASE;, mRNA
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                                                                    EST 14-JUL-2000
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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Marra,M., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Marra,M., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R. Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Possible reversed clone: similarity Seq primer: -40RP from Gibco High quality sequence stop: 338.

Location/Qualifiers
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Similarity 61.9%;
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                                                                                           AGCCTGACCAACAGTCT 504
                                                                                                                                        GCGCTGAGTAAATCTCT 257
                                                                                                                                                                                                                              GCTTCTCTCGGTGCTAATGCACGCCTGGTCGGGTTGACGGCATTGACGATGCAGCGCGC
                                                                                                                                                                                                                                                                              GTCAATGTCGAGCACATCGAGGATCGCCCCGGTGGTGCCGCCAACGTTGCCCTGAACATT
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                                                                                                                                                                                   GNCGCTCTGGGGGGCCCCGGCGTCGCTGGTGGGTGTCACCGGTGACGACTAGGCCGTCTAC
                                                                                                                                                                                                                                                                                                                                                                       CTCGACCGTTACTGGCATGGTGCTACCTCACGGATTTCTTCTGAGGCGCCGGTGCCTGTG
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314 286 1810
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/lab_host="DB10B (phage-resistant)"
/lab_host="DB10B (phage-resistant)"
/clone_lib="Perkins LRH"
/clone_lib="Perkins LRH"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Eag1; cDNA made by oligo-dT priming. Library amplified by stretch PCR. Subtraction method: Bonaldo, et al., Genome Research 6:791. Library constructed by Dr. Archibald Perkins (Yale University)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
/mol_type="mRNA"
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/clone="IMAGE:3216101"
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Pred. No. 1.7e-17;
0; Mismatches 98
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VERSION
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AUTHORS
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Zea mays
Unpublished (2002)
Other_GSSs: OGCAW49TM
Contact: Cathy Whitel:
                                                                                                                                                                                                                                                                           OGCAW49TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0130J01, genomic survey sequence. BZ648800
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1 (bases 1 to 226)
1 (bases 1 to 226)
1 (bases 1, Wan Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OGCAW49TM ZM 0.7 1.5 KB Zea mays genomic survey sequence.
BZ648805
                                                   1 (bases 1 to 251)
WhiteLaw, C.A., Quackenbush, J., Van Aken, S., Utterback, WhiteLaw, C.A., Quackenbush, J., Van Aken, S., Utterback, Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rcitek, R.W., Numberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
                                                                                                                                            Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Resnick,A., Fraser,C.M., Budiman,M
Citek,R.W., Nunberg,A., Robbins,D.
Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BZ648805.1
GSS.
                                                                                                                                                                                                                        Zea mays
                                                                                                                                                                                                                                       GSS
                                                                                                                                                                                                                                                          BZ648800.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: methylation filtered.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Cent
Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
Other_GSSs: OGCAW49TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCGTATGATTGTGCTGGGCGCGCACTGGAAGCGGTC 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
 Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4577"
/clone="zwMBMa0130J01"
/clone_il="zm_0.7 7.1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII;
methylation_filtered_genomic_DNA_librar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/mol_type="genomic_DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 226
                                                                                                                                                                                                                                                            GI:28112874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 96;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Lo
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                                                                                           Rohlfing, T.,
                                                                                                                                                                                                                                                                                                                                    GSS 29-JAN-2003
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RESULT 15
CN817146/c
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VERSION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Rines, H.W. USDA-ARS and University of Minnesota 1991 Upper Buford Circle, 411 Borlaug Hall, Tel: 612 625 5220 Pax: 612 625 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CN817146 TRANSCE TIPE TO THE TRANSCE TO THE TRANSCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rines, H.W., Anderson, O.D., Crossman, C.C., Lazo, G.R., Miller, S.S., Taller, J.M. and Vance, C.P.
ESTs from Avena sativa cv. Ogle-C roots, etiolated leaves, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Avena sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Avena sativa (oat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CN817146.1 GI:50358506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences have been trimmed to remove low quality sequence with phred scores less than 20 and most vector sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3mail: rines001@umn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coideae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methylation filtered
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/clone_lib="ZM_0.7_1.5 kB"
/note="Vector; pBCSK: 5 lte_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                               /organism="Avena sativa"
/mol_type="mRNA"
/culfivar="Ogle-C (a reselection from cv. Ogle)"
/db_xref="faxon:4498"
/clone="HRO4528 G04 N08"
/tissue_type="root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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                                                                                                                                                dev_stage="6-day-old"
lab_host="E. coli SOLR (excised)
                               clone lib="Lib AA071E1X Avena sativa cv. Ogle-C root" note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                                                                                                                 sequencing)
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Pred. No.
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germinated in a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 18-JUL-2004
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CIGCGIATCGATTICGAAGAGCCCTTCG 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dark incubator at 20 C. At 6 days roots were harvested, total RNA and poly(A) were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson USDA-ARS lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pBluescript phagemids in the HW Rines and CP Vance
USDA-ARS labs (Rines, Vance, Miller, Taller) at th
University of Minnesota, St. Paul, MN. Plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAG_LIB=AA071E1X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Albany, CA.
TAG_TISSUE=root
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Pred. No. 1.9e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 764;
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/P_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/P_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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3 US-09-489-039A-2037

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3 US-09-557-884-1

3 US-09-557-991A-16413

3 US-09-252-991A-16413

3 US-09-252-991A-1678

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1 US-09-902-540-8926

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                                                                                                                                                                                          Sequence 165, App
Sequence 2037, Ap
Sequence 2107, Ap
Sequence 2462, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 16413, A
Sequence 16304, A
Sequence 16178, A
Sequence 16175, A
Sequence 185, App
Sequence 952, App
Sequence 8926, App
Sequence 1, Appli
Sequence 186, App
Sequence 16071, Ap
Sequence 2497, Ap
Sequence 4496, Ap
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US-09-489-039A-585	US-10-114-170-179	US-09-453-702B-179	US-09-103-840A-1	US-09-103-840A-2	US-09-902-540-1209	US-09-902-540-4200	US-09-303-518D-747	US-09-902-540-1262	US-09-902-540-5380	US-08-232-463-14	US-09-252-991A-2891	US-09-103-840A-1	US-09-103-840A-2	US-09-489-039A-5586	US-09-252-991A-2707	US-09-252-991A-2978	US-09-252-991A-3080	US-09-949-016-2757	US-09-270-767-14850	US-09-270-767-31103	
Sequence 585, App	Sequence 179, App	Sequence 179, App	Sequence 1, Appli	Sequence 2, Appli	Sequence 1209, Ap	Sequence 4200, Ap	Sequence 747, App	Sequence 1262, Ap	Sequence 5380, Ap	Sequence 14, Appl	Sequence 2891, Ap	Sequence 1, Appli	Sequence 2, Appli	Sequence 5586, Ap	Sequence 2707, Ap	Sequence 2978, Ap	Sequence 3080, Ap	Sequence 2757, Ap	Sequence 14850, A	Sequence 31103, A	

ALIGNMENTS

RESULT 1 US-09-492-709A-165

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Ş	₽ <i>Q</i>	용 성	용 성	B <i>정</i>	Query Ma Best Loo Matches	; TY ; OR US-09-	SEQ ;	NOW COM	; TITLE ; TITLE	; APP ; APP	; APP	; APP	; Sequence ; Patent No ; GENERAL :
241 GCGCTGAGTAAATCTCTGGCCGACGTCAACGTCAAATGCGACTTCGTTTCTGTACCGACG	181 GCTTCTCCGGTGCTAATGCACGCCTGGTCGGGTTGACGGCATTGACGATGCAGCGCGCGC	121 GTTAAAGTGAATACCATCGAAGAACGTCCGGGCGGCGCGCGC	61 CTGGATCGTTACTGGTACGGCCCCACCAGTCGTATCTCGCCGGAAGCGCCGGTGCCCGTG	1 ATGAAAGTAACGCTGCCAGAGTTTGAACGTGCAGGAGTGATGGTGGTGGTGATGTGATG 	Query Match 100.0%; Score 1434; DB 3; Length 1434; Best Local Similarity 100.0%; Pred. No. 0; Matches 1434; Conservative 0; Mismatches 0; Indels 0;	TYPE: DNA ORGANISM: B. Coli 09-492-709A-165	FastSEQ for 165 1434		LE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION LE OF INVENTION: ESCHERICHIA COLI 3 REFERENCE: ELITRA,001A	APPLICANT: Carr, Grant J. APPLICANT: Yamamoto, Robert T. APPLICANT: Xu, H. Howard	Froel	APPLICANT: Zyskind, Judith APPLICANT: Ohlsen, Kari L. APPLICANT: Trawick John	Sequence 165, Application US/09492709A Patent No. 6720139 GENERAL INFORMATION:
GTACCGACG	rgacgatgcagcgcgc 	ATGAATATC	GTGCCCGTG	GATGTGATG	0; Gaps	·. ·	er j		ATION IN	٠.	<i>:</i>		
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              GCCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGAC
                                                      ATCGCCGGGATCTTGCCAGATCTGCTGGTGAAAGGCGGCGACTATAAACCAGAAGAGATT
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TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 2037
LEMOTH: 1500
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2037
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Best Local Similarity
Matches 1166; Conserv
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Pred. No. 5e-285;
0; Mismatches 257;
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KLEBSIELLA

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RESULT 3
US-09-489-039A-2107/c
Sequence 2107, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUPWONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NO 2107
SEQ ID NO 2107
LENGTH: 1323
TYPE: DNA
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                      <u>ĠĠCGTGATGAGCGAAGAGGAGCTCAAACAGGCGGTTGCGGCGGCGCGCGAAGCGCGGCGAG</u>
                                                                                                                                                                                          GAAGAGGCCTGCTATTTCGCTAACGCCGCGGCGGGCGTGGTGGTCGGTAAGCTGGGTACA
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Pred. No. 8.1e-244;
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APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEU

FILE REPERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 2462

LENGTH: 1476

TYPE: DNA

ORGANISM: Proteus mirabilis

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Best Local
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Pred. No. 4.7e-201;
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Sequence 1, Application US/0955
PATENT NO. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann e
TITLE OF INVENTION: The
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                                                                                                                                GGTATTTCCACAACTAATATTATTAATGCCATTAAAAAAGAAATAA
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER: BELL FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentlum
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII TEXT
CURRENT APPLICATION NUMBER: US/09/557,884
PILING DATE: 25-Apr-2000
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE, JOIL 301-309-5504
TELECOMMUNICATION INPORMATION:
TELEPHONE: 301-309-5504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1596554 CAGAATTTAAGCAAAGCAAAAGTACTCGTATTAGGCGACGTGATGCTTGATCGTTATTGGT 1596495
  1596134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1596434 ATGAAGAACGCGCGCGCTGCTGCAGCAAATGTGGCGATGAATATTGCTTCACTCAATGTAC 1596375
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                               257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 TCGAAGAACGTCCGGGCGCGCGCGCTAACGTGGCGATGAATATCGCTTCTCTCGGTGCTA 196
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  CTTTGATTCTTTCTGATTACGGCAAAGGCACGCTTAAAGATGTTCAGAAAATGATTCAAA 1596075
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                                                                                                 ATAATGTAGATTGCAAGGATTTATTAGCGAAGTTAGAAAGTGCGGTGAAAAATTACGGTG 1596135
                                                                                                                                               AAGGTGTTGATCCGCAGCCGCTGCACGAGCGGATTAATCAGGCGCTGAGTTCGATTGGCG 436
                                                                                                                                                                                                AATTACGTATTTTATCTCGTCATCAACAGCTGCTCCGCCTTGATTTTGAAGAAGATTTCA 1596195
                                                CGCTGGTGCTTTCTGACTACGCCAAAGGTGCGCTGGCAAGCGTACAGCAGATGATCCAAC 496
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                                                                                                                        RESULT 6
US-09-643-990A-1/c
Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Robert D. Fleischmann
Mark D. Adams
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TITCHCCHANGGGANTGTTGCCTGTTGTTGATCCATCCAAAGCTGATTGAACGTTAAAGCTGTTTGAACGTTAAAAGCTGATTTGAACGTTAAACGTTAAAAGCTGATTTGAACGTTAAACGTTAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACGTTAAAACAAAC	159	ру 159	Ду рь 159	ду рь 159	Ду ОБ 159	Ду рь 159	Ду Db 159	ду рь 159	Ду рь 159	ду рь 159	2y 0b 159	Ду Db 159	ду рь 159	Ду рь 159	ду 159
			1217 5354	1157 ATTC 95414 AAAG	1097 TGGG 595474 TGGG							677 5894			497 TGGC 96074 TTGC
	GGCAAACGGT	TCTGCTGGTC	CIGGGIAGIO CIGGIIGGIO	CCGCCCGGTA TCGCCCAATT	TGACCGCTTO	TGTCTTTGAC	ACTGAAGCTO 	GCTGGAAAA1 ACTTGAAAA1	CAATGCGGCC	TAGCGTATT	GCATATGCC! TCATTTGCC!	TCTGTTAGTO	GACCGAAGAJ TACGGAAGAJ	CGGCGCTACO	GCGTAAAGCC ACGCAAAGCC
	GGCGATGTTA ATCCAA 141	HAMAGGCGGCC	TCGTTTGAAG	AACCCACTCC	ATTGTTGCCC	ATCCTGCACC	GCTGTAGCGG	GCTGTACGTO	GCTGGCGTGG	GCAACCGCAT	VACCCAAGCGC ACTGTTGCAA	BACCCGTTCCC BACGCGTTCTC	GAGATTGTTG	CTGTTAACGO	AATGTGCCTG
	 \AAGTGCTAA .6	HOTATAAACO	AGGACACGCC AAGATACACC	BAACAGCGTAT	TCAACAGCG! TAAACAGCG!	CCGGGCACG	CAGCGCGTA PAAGCTAAAGC	GACGTGCAGA CTCGTCCTGA	TGGTCGGCAJ	TGGCAGCGGC TAGCAGATGC	AGGAAGTGTA AAGAAGTGTT	baacagggtat baaaaaggcat	bagcgcggcat bagaaaggttt	CGAATCTCTC CCAATATGTC	FIGURATION STREET
		CAGAAGAGAT	CGCAGCGCTT 	TGATTGTGCT	ATGCCTCCAC	CTCTTATCT	VACGTGGTGA)GCGCGGTGA	ATACAGGCTT	VACTGGGAAC VATTGGGGAC	TAATTCGCT	ATGACGTTAC	NGTCGCTGCTY 	rgaaactgat raaaattaat	GGAATTTGA TGAATTTGA	ATCCAAAAGG
	 TGGTTGTTCA	TGCCGGGAGI	GATCGCCGGG AATCGGCGAA	GGCGCACTG	CAAACGGCTG TAAACGCTTA	GGCAAATGCC NGAAAATGCA	aaaagtggtg aaaaattgtg	resceteate rescattate	CTCCACGGTT TCAACGGTT	GGAAGAAGCC GAAGAATCT	ceereceec geaaccceer	GCAACCGGGT ACGCCCAAAT	TGCCGATTAC	AGCTGTTGTC	TACCGATTTT NACTGATTTT
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Best Local Similarity 65.9%;
Matches 922; Conservative
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SEQUENCE CHARACTERISTICS:
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Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd
Thereof, and Uses Thereof
                                                                                                                                                                                                                                   1596374 CCGTTCAGTTAATGGGATTGÁTTGGACAAGÁTGÁAACTGGTTCTGCACTTTTCCCTCTTAT 1596315
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APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:

NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEPHONE: 301-610-5790
                                             1596254 AATTACGTATTTTATCTCGTCATCAACAGCTGCTCCGCCTTGATTTTGAAGAAGATTTCA 1596195
                                                                                                                                         1596314
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION UNMEER: US/09/643,990A

PILING DATE: 23-Aug-2000

CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO:
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CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
                                                                                                                                                                                                                                                                                 197
                                                                                                                                                                                                                                                                                                                                                              77 ACGGCCCACCAGTCGTATCTCGCCGGAAGCGCCGGTGCCCGTGGTTAAAGTGAATACCA 136
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AAGGTGTTGATCCGCAGCCGCTGCACGAGCGGATTAATCAGGCGCTGAGTTCGATTGGCG 436
                                                                                                                                         TAGAAAAAAAAAAATTGATTGTAATTTTGTTGCATTAGAAACCCATCCAACCATTACTA 1596255
                                                                                                                                                                                                                                                                            AATTACGGGTACTTTCCCGCAACCAACAGCTGATCCGTCTGGATTTTGAAGAAGGTTTCG 376
                                                                                                                                                                                     TGGCCGACGTCAACGTCAAATGCGACTTCGTTTCTGTACCGACGCATCCGACCATTACCA 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 635.2; DB 3; Length 1830121; 
Pred. No. 1e-173; 
0; Mismatches 478; Indels 0; G
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ACATCATCAAGAAGATCCAA 1416	1397 ACATCATCAAG	Ş
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TCGACTGGGTAGTGTCGTTTGAAGAGGACACGCCGCAGCGCTTGATCGCCGGGATCTTGC 1276	1217 TCGACTGGGTA	8
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TGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCCTCCACCAAACGGCTGAAAGGGG 1156	1097	\$ \$
		Db .
3GTGTCTTTGACATCCTGCACGCCGGGCACGTCTCTTATCTGGCAAATGCCCCGCAAGC 1096	1037 ACGGTGTCTTT	S S
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AGGAACTGAAGCTGGCCGTAGCGGCAGCGCGTAAACGTGGTGAAAAAGTGGTGATGACCA 1036	977 AGGAACTGAAG	ई
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TCGAGCTGGAAAATGCTGTACGTGGACGTGCAGATACAGGCTTTGGCGTGATGACCGAAG 976	917 TCGAGCTGGAA	S
TIGCCAATGCGGCGGCTGGCGTGGTGGTCGGCAAACTGGGAACCTCCACGGTTTCGCCGA 916	857 TTGCCAATGCG 1595714 TAGCCAATGTT	B 정
TCATTAGCGTATTAGCAACCGCATTAGCAGATGGACGTTCTTTCGAAGAATCTTGTTACC 1595715	1595774 TCATTAGCGTA	뫄
TGATIGGCGICCIGGCAGCGGCAGCGGGTAATICGCIGGAAGAAGCCIGCTICI 856	797 TGATTGGCGTC	ğ
CTTATCATTTGCCAACTGTTGCAAAAGAAGTGTTTGATGTGACGGGAGCCGGTGACACTG 1595775	1595834 CTTATCATTTG	ф
CGCTGCATATGCCAACCCAAGCGCAGGAAGTGTATGACGTTACCGGTGCGGGGGGACACGG 796	737 CGCTGCATATG	Ş
CCGCTCTGTTAGTCACCCGTTCCGAAAAAGGCATGACATTATTACGCCCAAATCAAGAGC 1595835	1595894 CCGCACTTING	B &
15		D.
	617	Q
DGTGGGGCTACATTATTGACACCCAATATGTCTGAATTTGAAGCTGTTGTGGGTAAAT 1595955	1596014 ATCGTGGGGCT	Дb
ACCGCGGCGCTACGCTGTTAACGCCGAATCTCTCGGAATTTGAAGCTGTTGTCGGTAAAT 616	557 ACCGCGGCGCT	Ş.
TIGCACGCAAAGCGAATGIGCCTGTGTTGATCGATCCAAAGGGAACTGATTTTGAACGTT 1596015	1596074 TTGCACGCAAA	Дb
TGGCGCGTAAAGCGGGTGTTCCGGTGCTGATTGATCCAAAAAGGTACCGATTTTGAGCGCT 556	497 TGGCGCGTAAA	§
CTTTGATTCTTTCTGATTACGGCAAAGGCACGCTTAAAGATGTTCAGAAAATGATTCAAA 1596075	1596134 CTTTGATTCTT	Db
CGCTGGTGCTTTCTGACTACGCCAAAGGTGCGCTGGCAAGCGTACAGCAGATGATCCAAC 496	437 cecreerecri	δ
1596194 ATAATGTAGATTGCAAGGATTTATTAGCGAAGTTAGAAAGTGCGGTGAAAAATTACGGTG 1596135		Db

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US-10-158-865-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPPLICANT: Pleischmann et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENERAL INFORMATION:
                                                                                                   NAME/KEY: misc feature
LOCATION: (44975)...(44975)
DTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAME/KEY: misc_feature
LOCATION: (10150)..(10150)
WITHER_INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JRRENT FILING DATE:
                               NAME/KEY: misc_feature
.OCATION: (45593)..(45593)
THER INFORMATION: n equals a,t,c,
                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
OCATION: (40808)..(40810)
THER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OCATION: (36636)..(36636)
THER INFORMATION: n equals
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.OCATION: (36551)..(36551)
THER_INFORMATION: n equals
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OCATION: (44416)..(44416)
THER INFORMATION: n equals
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OCATION: (36543)..(36543)
THER INFORMATION: n equals a,t,c,
                                                                                                                                                                         AME/KEY: misc_feature
OCATION: (44905)..(44905)
THER INFORMATION: n equal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCATION: (4747)..(4747)
THER INFORMATION: n equals
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CATION: (4747)...(474
ME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/426,787 FILING DATE: 1995-04-21
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5. 6846651
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NAME/KEY: misc_feature
LOCATION: (119924)..(119924)
OTHER_INFORMATION: n equals
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LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals
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LOCATION: (80024)..(80024)
OTHER INFORMATION: n equal
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LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals
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LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals
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LOCATION: (51602)..(51602)
OTHER INFORMATION: n equals
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equal
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OTHER INFORMATION: n equals
                                               NAME/KEY: misc_feature
LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals
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LOCATION: (100091)..(100091)
OTHER INFORMATION: n equals
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LOCATION: (65313)..(65313)
OTHER INFORMATION: n equals
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LOCATION: (51786)..(51786)
OTHER_INFORMATION: n equals
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OTHER INFORMATION: n equals
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                                                                                                                                                                                               NAME/KBY: misc_feature
LOCATION: (119750)..(119750)
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LOCATION: (102696)..(102696)
DTHER_INFORMATION: n equals
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JOCATION: (51805)..(51805)
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misc_feature (121344)..(121344)
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Best Local Similarity
Matches 922; Conserval
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NAME/KEY: misc_feature
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a,t,c, or
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (147197)...(147197)
OTHER INFORMATION: n equals
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LOCATION: (145942)..(145942)
OTHER_INFORMATION: n equals a,t,c,
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LOCATION: (14571)..(145171)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature

LOCATION: (131360)..(131360)

OTHER INFORMATION: n equals a,t,c,
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (122336)..(122336)

OTHER INFORMATION: n equals a,t,c,
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals
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                               1596434 ATGAAGAACGCGCGGGTGCTGCAGCAAATGTGGCGATGAATATTGCTTCACTCAATGTAC 1596375
                                                                                             1596494 TCGGCGCAACCAACCGTATTTCACCAGAAGCACCAGTACCAGTGCTTCGTGTACAAGAAA 1596435
                                                                                                                                                             1596554
                                                               137
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                                                                                                                           77 ACGGCCCCACCAGTCGTATCTCGCCGGAAGCGCCGGTGCCCGTGGTTAAAGTGAATACCA 136
                                                     CAGAATTTAAGCAAAGCAAAAGTACTCGTATTAGGCGACGTGATGCTTGATCGTTATTGGT 1596495
                                                                                                                                                                               CAGAGTTTGAACGTGCAGGAGTGATGGTGGTTGGTGATGCTGGATCGTTACTGGT 76
Conservative
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                                                                                                                                                                                                                       Score 635.2; DB 3; Pred. No. 1e-173; 0; Mismatches 478;
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PILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16413
LENGTH: 1581
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US-09-252-991A-16413
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
PILE REFERENCE: 107196.136
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Best Local Similarity
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ORGANISM: Pseudomonas aeruginosa
-09-252-991A-16413
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; Sequence 16304, Application US/09252991A
; Patent No. 6551795
; Patent No. 6551795
; GENERAL INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
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PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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LENGTH: 1251
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                                                                                                   GCCGTGCTGGGCCTGGAGCAATTGCTGCTGGCAATCGAAGACGCCCGCGCCCCACGGCGAG
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Pred. No. 8.5e-104;
0; Mismatches 445;
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ACTCGCCTGAAGGGCGTTGGCCGGCCGATCAACTCGGTGGACCGGCGCATGGCGGTACTC

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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16178
PRIORIE: 963
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US-09-252-991A-16178/c
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Best Local :
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ORGANISM: Pseudomonas
-09-252-991A-16178
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
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 TCCACGGTTTCGCCGATCGAGCTGGAAAATGCTGTACGTGGACGTGCAGATACAGGCTTT
                                    CCGTCCGCGGTGGGCCTGGCCAACCTGGCCGGCATCGTGGTCGGCAAGCTGGGTACC
                                                                    GAAGAAGCCTGCTTCTTTGCCAATGCGGCGGCTGGCGTGGTGGTCGGCAAACTGGGAACC
                                                                                                      GGTGCCGGCGATACGGTCATCTCCACCCTGGCCGCGGCGCTTGCCGCCGGCGAGGAGCTG
                                                                                                                                    GGTGCGGCGACACGGTGATTGGCGTCCTGGCGGCAACGCTGGCAGCGGGTAATTCGCTG
                                                                                                                                                                                                      CAACCGGGTAAAGCGCCGCTGCATATGCCAACCCCAAGCGCAGGAAGTGTATGACGTTACC
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Pred. No. 6.2e-92;
0; Mismatches 368;
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FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOPTWARE: PATENTIN VET: 2.1
SEQ ID NO 1
LENGTH: 640681
TYPE: DNA
DORGANISM: Buchnera sp.
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US-09-790-988-1/c
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Patent No. 6632935
GENERAL INFORMATION:
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL
                                                                                                                                                                                                                                                                       09-790-988-1
                                                                                                                                                                                        y match
Local Similarity 53.4%;
res 500; Conservative
                                                       65998 CTAGATTGTTATTGGTATAGCAAAAATCACTATATGCTATCTGAACAATTAACACCAATT
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                                                                                  CTGGATCGTTACTGGTACGGCCCCACCAGTCGTATCTCGCCGGAAGCGCCGGTGCCCGTG
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                                                                                                                                                                                             Score 238.4; DB 3;
Pred. No. 4.7e-58;
0; Mismatches 436;
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GAAACATTGAATATTAATGAGTTAAATTCTGTTTTA 65123
                                                                                                       GAAGAAGCCTGCTTCTTTGCCAATGCGGCGGCGGCGTGGTGGTCGGCAAACTGGGAACC
                                                                                                                                          GGTGCAGGAGATACAGTGATCGCTATAATTGCAGCATCTTTAGCAACTGGATATTCTTTA
                                                                                                                                                                                                                CAAAAAGAAAAAAACCAATACATTTTCCTGCCGCATCTAAAATAGCTTCAGATGTAACT
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                               TCCACGGTTTCGCCGATCGAGCTGGAAAATGCTGTA 936
                                                                    GAAGAAGCTTGTTTTATGCCAATATTGGAGCCAGTATTGTTATACAGAAAATTGGAACT 65159
                                                                                                                                                                          GGTGCGGCGACACGGTGATTGGCCTCCTGGCGGCAACGCTGGCAGCGGGTAATTCGCTG
                                                                                                                                                                                                                                                  CAACCGGGTAAAGCGCCGCTGCATATGCCAACCCCAAGCGCAGGAAGTGTATGACGTTACC
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RESULT 12
US-09-252-991A-15975/c
US-09-252-991A-15975/c
US-09-252-991A-15975/c
Sequence 15975, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
PILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILLING DATE: 1998-07-27
NUMBER OF SEQ ID NO 15975
LENGTH: 501
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RESULT 13
US-08-651-155B-185
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                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6365401
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 185,
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ORGANISM: Pseudomonas aeruginosa
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
LIVER SYSTEM DATE: 17-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                     APPLICANT: Mahan Dr., Michael J.
APPLICANT: Conner Mr., Christopher P.
APPLICANT: Hiethoff Mr., Douglas M.
TITLE OF INVENTION: METHOD AND PROBES FOR THE IDENTIFICATION
TITLE OF INVENTION: OF MICROBIAL GENES SPECIFICALLY INDUCED DURING
TITLE OF INVENTION: INVECTION
NUMBER OF SEQUENCES: 255
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Chrisman, Bynum & Johnson,
STREET: 1900 Fifteenth Street
                                                                                                                                                                                                STATE:
                                                                                                                                                             COUNTRY: U
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Similarity 59.5%;
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    Mismatches

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Pred. No. 3e-41;
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; HYPOTHETICAL: NO;
; ANTI-SENSE: YES
US-08-651-155B-185
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US-09-194-036B-185
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                                                                                                                                                                                                                                                                                                Sequence 185, Application US/09194036B Patent No. 6548246 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 347 base pairs
TYPE: nucleic acid
STRANDEDWESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Petersen Mr., Steven (
REGISTON NUMBER: 36,238
REFERENCE/DOCKET NUMBER: 17/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/546-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11
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          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                   APPLICANT: Mahan, Michael J.
Conner, Christopher P.
Hiethoff, Douglas M.
TITLE OF INVENTION: METHOD AND PROBES FOR THE IDENTIFICATION
OF MICROBIAL GENES SPECIFICALLY INDUCED DURING
                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEB: Morrison &
STREET: 755 Page Mill
CITY: Mountain View
CURRENT
                                                                                                                                                                                            NUMBER OF SEQUENCES:
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240; Conserv
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                                                                                      ZIP: 94304
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APPLICATION DATA:
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Pred. No. 1.7e-33;
0; Mismatches 76
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               Version
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/194,036B FILING DATE: 17-No. 6548246-1998 CLASSIFICATION: <Unknown>

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RESULT 15
US-09-252-991A-16179/c
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; SEQUENCE DESCRIPTION: SEQ ID NO: 185:
US-09-194-036B-185
Sequence 16179, Application US/09252991A
patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILLING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US/60/074,788
PRIOR APPLICATION NUMBER: US/60/094,190
PRIOR APPLICATION NUMBER: US/60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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REFERENCE/DOCKET NUMBER: 220
TELECOMMUNICATION INFORMATION:
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FILING DATE: 1997-05-16
APPLICATION NUMBER: US 08/651,155
FILING DATE: 1996-05-17
ATTORNEY/AGENT INFORMATION:
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240; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No. 1.7e-33;
0; Mismatches 76;
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; SEQ ID NO 16179

LENGTH: 789

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-16179
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Best Local Similarity 58.3%;
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Pred. No. 5.3e-32;
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Search completed: March 18, 2006, 19:21:03 Job time : 469 Becs

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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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7440.5
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1: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/USO1 NEW PUB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/USO1 NEW PUB.pep:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                    US-10-520-820-13
US-10-467-657-3254
US-11-098-686-11061
US-11-098-686-10264
US-11-096-568A-6281
US-11-096-568A-31211
US-11-096-568A-31211
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US-11-096-568A-31089
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US-11-096-568A-31089
US-11-096-568A-31089
US-11-096-568A-10265
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                       Sequence 13, Appl
Sequence 2548, Ap
Sequence 11061, Ap
Sequence 10264, A
Sequence 7, Appli
Sequence 6281, Ap
Sequence 31212, A
Sequence 31211, A
Sequence 31211, A
Sequence 31089, A
Sequence 10266, A
Sequence 10266, A
Sequence 10266, A
Sequence 10267, A
Sequence 10267, A
Sequence 9229, App
Sequence 9239, App
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US-10-520-820-13
(Sequence 13, Application US/10520820
Publication No. US20060003393A1
GENERAL INFORMATION:
APPLICANT: MUTABILIS S.A.
TOTAL OF INVENTION: Pathogenicity di
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	880, App	Sequence	US-11-087-099-880	7	319	4.4	106	45
	9, Appli	Seguence	US-11-175-689-9	7	14130	4.5	106.5	44
	4598, Ap	Sequence	US-10-467-657-4598	0	537	4.5	106.5	43
	7, Appli.	Sequence	US-11-075-185-7	7	3507	4.5	107	42
	22, Appl	Sequence	US-10-840-688-22	6	592	4.5	107	41
	786, App	Sequence	US-10-793-626-786	σ	319	4.5	107	40
	7465, Ap	Sequence	US-11-087-099-7465	7	325	4.5	107.5	39
	6628, Ap	Sequence	US-10-467-657-6628	σ	633	4.5	108	38
	4364, Ap	Sequence	US-11-087-099-4364	7	335	4.5	108.5	37
٠.	10, Appl	Sequence	US-11-082-389-10	7	524	4.6	109	36
	8532, Ap	Sequence	US-11-087-099-8532	7	1121	4.6	110.5	35
	2, Appli	Sequence	US-11-052-554A-2	7	1571	4.7	112	34
	34249, A	Sequence	US-11-096-568A-34249	7	371	4.8	116	ω W
٠.	31151, A	Sequence	US-11-096-568A-31151	7	404	4.9	116.5	32
	31152, A	Sequence	US-11-096-568A-31152	7	372	4.9	116.5	31
:	31753, A	Sequence	US-11-096-568A-31753	7	314	4.9	118	30
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	31752, A	Sequence	US-11-096-568A-31752	7	343	5.2	123.5	28
	1705, Ap	Sequence	US-11-087-099-1705	7	325	5.2	123.5	27
	19, Appl	Sequence	US-11-201-916-19	7	545	5.2	125.5	26
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ALIGNMENTS

TITLE OF IN THE REFERE CURRENT FILL PRIOR APPLLI PRIOR FILLIN TUPE: PRI TYPE: PRI T	TITLE OF INVENTION: means for preventing and controlling bacterial TITLE OF INVENTION: dissemination PILE REFERENCE: 1621 CURRENT APPLICATION NUMBER: US/10/520,820 CURRENT PILING DATE: 2005-01-07 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: US/10/520 A	TITLE OF INVENTION: Pathogenicity determinants which can be used TITLE OF INVENTION: dissemination preventing and controlling bacter: TITLE OF INVENTION: UNMBER: US/10/520.820 CURRENT APPLICATION NUMBER: US/10/520.820 PRIOR APPLICATION NUMBER: PCT/EP2003/008209 PRIOR APPLICATION NUMBER: PCT/EP2003/008209 PRIOR APPLICATION NUMBER: PCT/EP2003/008209 PRIOR FILING DATE: 2002-07-09 PRIOR PILING DATE: CO. 09 PRIOR PILING DATE: CO. 0						·				
TITLE OF IN THE PRIOR APPLLI PRIOR APPLLI PRIOR APPLLI PRIOR FILLIN UNDER OF S SOPTWARE; F TYPE: PT	TITLE OF INVENTION: means for preventing and controlling bacterial TITLE OF INVENTION: dissemination PILE REFERENCE: 1621 CURRENT APPLICATION NUMBER: US/10/520,820 CURRENT PILING DATE: 2005-01-07 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: PR 0208636 PRIOR PILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: US/10/520 A	TITLE OF INVENTION: Pathogenicity determinants which can be used as TITLE OF INVENTION: dissemination preventing and controlling bacterial TITLE OF INVENTION: dissemination Proventing and controlling bacterial CITLE OF INVENTION: dissemination Price Repersion 1621 CURRENT FILING CATTON NUMBER: US/10/520,820 CURRENT FILING DATE: 2003-00-09 PRIOR PILING DATE: 2003-07-09 PRIOR PILING DATE: 2002-07-09 RIMBER OF SEQ ID NOS: 32 SOFTWARE: Patentin version 3.1 SEQ ID NO 13 LENGTH: 477 TYPE: PRI ORGANISM: Escherichia coli -10-520-820-13 Query Match 100.0%; Score 2393; DB 6; Length 477; Best Local Similarity 100.0%; Pred. No. 25e-164; Matches 477; Conservative 0, Mismatches 0; Ga 1 MKVTLPEFERAGYMYVGDVMLDRYWYGDTSRISPEAPVEVKVNTIEERPGGAANVA 61 ASIGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLI			•			•		-	•	
enting 20,820 3/0082 6 6 3/0082 6 6 23/0082 6 18 marco 18	nd controlling bacterial nd controlling bacterial DB 6; Length 477; Se-164; 0; Indels 0; Ga SPEAPVPVVKVNTIEERPGGAANVA SPEAPVPVVKVNTIEERPGGAANVA CDFVSVPTHPTITKLRVLSRNOQLI	nd controlling bacterial nd controlling bacterial controlling bacterial left to bact	241	181 181	121 121	61 61	4 4	atch 100.0%; Sc cal Similarity 100.0%; Pr 477; Conservative 0;	cherichia	PLICATION LING DATE: P SEQ ID N : Patentir 13	~ ~ ~ ~	

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CURRENT APPLICATION NUMBER: US/10/467,657; CURRENT FILING DATE: 2003-08-11; PRIOR APPLICATION NUMBER: GB-0103424.8; PRIOR FILING DATE: 2001-02-12; NUMBER OF SEQ ID NOS: 9218; SOFTWARE: SegWin99, version 1.04; SEQ ID NO 3254; LENGTH: 320; TYPE: PRT; ORGANISM: Neisseria gonorrhoeae; US-10-467-657-3254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
US-10-467-657-3254
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Sequence 11061, Application US/11098686
Publication No. US20060024698A1
GENERAL INFORMATION:
APPLICANT: Kapur, Vivek and Gebhart, Control of INVENTION: NUCLEIC ACID AND PROPERTY OF TITLE OF INVENTION: NUCLEIC ACID AND P
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APPLICANT: CHIRON SPA
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Aest Local Similarity
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APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
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                                                                                                                                                                                                                                                                                                                                                194
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51.0%; Pred. No. 3.3e-46;
tive 48; Mismatches 102;
    Connie J. POLYPEPTIDE
      SEQUENCES
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CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 548
LENGTH: 169
                                                                                                                                                                                                                                                                                                   Sequence 548, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrasia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NU
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                                                                               US-10-467-657-548
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CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: PRSTSEQ for Windows Version 4.0
SEQ ID NO 11061
LENGTH: 345
TYPE: PRT
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Best Local Similarity
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   Matches
                                     Query Match
                                                                                                                                                                                                                                                                                           FILE REFERENCE:
                                                                                         TYPE: PRT
ORGANISM: Neisseria
                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 Y---RGATLLTPNLSEFEAVVGKC-----KTEEEIVERGMKLIADYELSALLVTRSEQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 QPLHERINQALSSIGALVISDYAKGALASVQ-----QMIQLARKAGVPVLIDPKGTDFER 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 VGQDQSGEKIQDLLSTRGILSSIITFANRQTTVKTRVMAHRQQMIRLDHEESTSYNSKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 VLVVGDIMLDNYLIGVSDRISPEAPVPIVKIENEKQSLGGAGNVARSIAALGGKVTIIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 TGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEE--GFEGVDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVGTATVSPDELEEAI 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLGTSTVSPIELENAV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WALFLSPKKIWHIPTVGRDVFDVTGAGDTVIATFGLALSAGLDPLISAILANYAAGVVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMVLSNFEKYVSQHEIIILSDYNKG-LVSKEFMLGFQDILLAKNPNAKVLIDPRPCNIMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YALCKNIFALTPNTKE----TGECAGGMATSSQPELLAAGHTIMKLLSTKHLLTTLGDSG
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                             gonorrhoeae
14.3%; Score 341.5; DB (51.8%; Pred. No. 1.1e-17)
tive 21; Mismatches 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.1%; Score 480.5; DB 7; 37.0%; Pred. No. 3.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 127;
                                                                                                                                                                                                                                                                                                             NUCLEIC
                                       DB 6;
   44;
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                                       Length
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                                         169;
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Gaps
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APPLICANT: Jinrul Shi
APPLICANT: David Extl
APPLICANT: Lisa Hagen
APPLICANT: Hongyu Wang
TITLE OF INVENTION: Polynucleotides and Methods of Use
FILE REFERENCE: 035718/291638
FULE REFERENCE: 035718/291638
CURRENT APPLICATION NUMBER: US/11/132,864
CURRENT FILING DATE: 2005-05-19
PRIOR APPLICATION NUMBER: 60/573,000
PRIOR PILING DATE: 2004-05-20
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US-11-098-686-10264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Lawsonia intracellularis
US-11-098-686-10264
                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/11132864
Publication No. US20050289670A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.6%; Score 324.5; DB 7; Length 169; Best Local Similarity 46.1%; Pred. No. 1.9e-16; Matches 65; Conservative 27; Mismatches 48; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOPTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 10264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10264, Application US/11098686 Publication No. US20060024696A1
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR PILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR PILING DATE: 2002-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
  SOPTWARE: PastSEQ for Windows Version 4.0 EQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 11433
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TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 RKRGEKVVMTNGVFDILHAGHVSYLANARKIGDRLIVAVNSDASTKRL-KGDSRPVNPLE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLPFLEGHSTSGLVQKIRNKK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRAFVLAHLELIDFIIGFEEDTPLQLIEAIQPNVLVKGGDWCVEQIIGKEFVERNNGLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSNGKKIIFTNGCYDILHPGHLDLLTRAKTYGDILVLGLNTDNSVKRLGKDPDRPFNPFH 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTSTTKTLAKIRAAEGG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCSTINIIKKIQQDKKG
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                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature; LOCATION: (1)..(361); OTHER INFORMATION: Ceres Seq. US-11-096-568A-6281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-096-568A-6281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 6281
LENGTH: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
TITLE OF INVENTION: Therby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6281, Application US/11096568A Publication No. US20060048240A1
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 9.6%; Score 229.5; DB 7 Local Similarity 29.2%; Pred. No. 3.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 -VIGVLAATLAA------GNSLEEACFFANAAAGVVVGKLGTSTVSP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 EVEEALAALHKLLAKGAVTKLVVVTLGADGALLVTKG-GEVHVPAVPKVKVVDTTGAGDA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 RNQQLIRLDFEEGFEGVD-------PQPLHERINQALSSIGALVLSDYAKGALAS 159
                                                                                            107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 RLVGLTGIDDAARALSKSLADVNVKCDFVSVPT------HPTITKLRVLS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 VMVVGDVMLDRYWYGPTSRISPBAPVPVVKVNTIBERPGGA-ANVAMNIASLG----ANA 67
                                                                                                                                        67 ARLVGLTGIDDAARALSKSLADVNVKCD----FVSVPTHPTITKLRVLSRNQQLIRLDFE 122
                                                                                                                                                                                      56 VVVVGSANAD--IYVEVDRLPGEG-----ETLAARSGQTIAGGKGANQATCSAKLAYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 AFIGKVGDDEFGEFLLELLKKEGVDTDYVKVDEGTRTGLALVLVDGDGGERTIVFYRGAN 117
                                                                                                                                                                                                                                  13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERP-----GGAANVAMNIASLGAN 66
                                                                                                                                                                                                                                                                                85;
                                           EGFEGVD----PQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TESEIVERGMKLIADYELSAL-LVTRSEQGMSLLQPGKAPLHMPTQAQ-EVYDVTGAGDT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVVIGEANIDLI---PTVEGLPEGELN-ERVKSFEKGPGGAGANVAVALARIGNPSYGKV 57
--IGGANLSCWPSSLPRQHLDLVAQAGIVLLQREIPDAVNA--QVAQAAKNAGVPVVLDA 217
                                                                                         TYFVGQVGDDAYGRLVTAGLRGGGVRLDNLAVVASAATGHAVVMLQSNGQNSIVY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQQMIQLARKAGVPVLIDPKGTD------FERYRGATLLTPNLSEPEAVVGKCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVAGFLAGLLATDDSNTQLDGKDLEBALRFANAAAALVVQKKGAISSLF 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----AAKAGGKISFDPNLRDPLWSDEBALEVLLELLPLADILKPNEEELELLTGLKG
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                   7.7%; Score 183.5; DB 7; 27.0%; Pred. No. 7.4e-06;
                                                                                                                                                                                                                                                                             41; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                  ID no.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 323;
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RESULT 9
US-11-096-568A-31212
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US-11-096-568A-6280
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Sequence 31212, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
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SEQ ID NO 6280
LENGTH: 369
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APPLICANT: Alexandrov, Nickolai et al.
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Best Local
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ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(369)
OTHER INFORMATION: Ceres Seq. II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Therby FILE REFERENCE: 2750-1592PUS2 CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT FILING DATE: 2005-04-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85;
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                                                                                                                                                                                        ACLCVQVKGASPSMP 357
                                                                                                                                                                                                                                                         LGHKGSALFVEGEKTIQQPAILAKTVVDTTGAGDTFTAAFAVALVEGKSKKECLRFAAAA
                                                                                                                                                                                                                                                                                        RSEQGMSLLQPGKAPLHMPT-QAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAA
                                                                                                                                                                                                                                                                                                                                                                                          --IGGANLSCWPSSLPRQHLDLVAQAGIVLLQREIPDAVNA--QVAQAAKNAGVPVVLDA
                                                                                                                                                                                                                                                                                                                                                                                                                           EGFEGVD----PQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARLVGLTGIDDAARALSKSLADVNVKCD----FVSVPTHPTITKLRVLSRNQQLIRLDFE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVVVGSANAD -- IYVEVDRLPGEG-----ETLAARSGQTIAGGKGANQATCSAKLAYP
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                                                                                                                                                                                                                                                                                                                           GGMDGPLPPQLINFVDILSPNETELARLTGMPTESFEEIQQAALKC---
                                                                                                                                                                                                                                                                                                                                                          KGTDF----ERYRGATLLTPNLSEFEAVVG-KCKTEBEIVERGMKLIADYELSA--LLVT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYFVGQVGDDAYGRLVTAGLRGGGVRLDNLAVVASAATGHAVVMLQSNGQNSIVY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSEQGMSLLQPGKAPLHMPT-QAQEVYDVTGAGDTVIGVLAATLAAGNSLEBACFFANAA 290
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Pred. No. 7.7e-06;
11; Mismatches 146;
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TYPE: PRT

GRANISM: Arabidopsis thaliana
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(378)
OTHER INFORMATION: Ceres Seq. ID no
US-11-096-568A-31212
                                                                                                                                                                                                            US-11-096-568A-31211
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CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 31211
LENGTH: 379
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CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 31212
LENGTH: 378
                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31211, Application US/11096568A Publication No. US20060048240A1
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Best Local Similarity
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                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)..(379)
OTHER INFORMATION: Ceres Seq. ID no. 13579028
                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 -----VGGANMKAWPEIMSDDDLEIVRNAGIVLLQREIPDSINI--QVAKAVKKAGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 RLDFEEGFEGVD----PQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 MYPTYFVGRLGEDAHGKLIAEALGDDGCGVHLDYVRSVNNEFTGHAVVMLQSDGQNSIII
                                           9
64 GANARLVGLTGIDDAARALSKSLAD--VNVKCDFV-SVPTHPT---ITKLRVLSRNQQLI
                                                                                28 PTSRISPEAPVPVVKVNT-----IEBRP----
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                                           PKSAVDAHAP-PLVVVGSANADIYVEIERLPKEGETISAKTGQTLAGGKGANQAACGAKL
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                                                                                                                         7.6%; Score 181.5; DB 7; 25.6%; Pred. No. 1.1e-05; tive 45; Mismatches 142;
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US-11-096-568A-31090
US-11-096-568A-31090; Sequence 31090, Application US/11096568A; Publication No. US20060048240A1; GENERAL INFORMATION:
RESULT 12
US-11-096-568A-31089
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CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 31090
LENGTH: 705
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
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LOCATION: (1). (705)
COTHER INFORMATION: Ceres Seq. ID no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thalians
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                                                                                                                                                                                 VTRSEQGMSLLQPGKAPLHMP-TQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFAN 288
                                                                                                                                                                                                                                                                                             -----VGGANMKAWPEIMSDDDLEIVRNAGIVLLQREIPDSINI--QVAKAVKKAGVP
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                                                                       AAASLCVQVKGAIPSMP
                                                                                                            AAAGVVVGKLGTSTVSP 305
                                                                                                                                            VKLGSKGSALFIQGBKPIQQSIIPAAQVV
                                                                                                                                                                                                                    VILDVGGMDTPIPNELLDSIDILSPNETELSRLTGMPTETFEQISQAVAKCHKLGVKQVL
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25.6%;
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Pred. No. 2.7e-05;
15; Mismatches 142;
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NAME/KEY: misc feature
LOCATION: (1)...(750)
OTHER INFORMATION: Cero
US-11-096-568A-31088
                                                                                                                                                                                                     FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 31088
LENCTH: 750
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA
TITLE OF INVENTION: Therby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31088, Application US/11096568A Publication No. US20060048240A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 31089
LENGTH: 741
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Query Match
Best Local Similarity
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NAME/KRY: misc feature
LOCATION: (1) - (741)
OTHER INFORMATION: Ceres Seq.
-11-096-568A-31089
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CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT ELLING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Sequence-Determined TITLE OF INVENTION: Therby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                 FEATURE:
                                                                                                                                                                                  ORGANISM: Arabidopsis thalians
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Local Similarity 25.6%;
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7.6%;
25.6%;
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Pred. No. 2.9e-05;
                                                                                           ID no.
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Score 181.5; DB Pred. No. 3e-05;
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US-11-096-568A-31213
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TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 31213
LENGTH: 261
TYPE: PRT
ORGANISM: Arabidopsis thaliana
PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(261)
OTHER INFORMATION: Ceres Seq. ID no. 13579030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31213, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                             124 GFEGVD----PQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPK 179
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                                                                                                                                                                                                                            61 -VGGANMKAWPEIMSDDDLEIVRNAGIVLLQREIPDSINI--QVAKAVKKAGVPVILDVG 117
                                                                                                                                                                                                                                                                                                                                      70 VGLTGIDDAARALSKSLAD--VNVKCDFV-SVPTHPT---ITKLRVLSRNQQLIRLDFEB 123
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                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                     VGKLGTSTVSP 305
                                                                      GSALFIQGEKPIQQSIIPAAQVVDTTGAGDTFTAAFAVAMVEGKSHEECLRFAAAAASLC 237
                                                                                                            GMSLLQPGKAPLHMP-TQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVV 294
                                                                                                                                               GMDTPIPNELLDSIDILSPNETELSRLTGMPTETFEQISQAVAKCHKLGVKQVLVKLGSK 177
                                                                                                                                                                                      GTDF----ERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQ 235
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 VQVKGAIPSMP 248
                                                                                                                                                                                                                                                                                                       VGRLGEDAHGKLIAEALGDDGCGVHLDYVRSVNNEPTGHAVVMLQSDGQNSIII-----
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                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                           6.9%; Score 166; DB 7; Length 261; 25.9%; Pred. No. 8.4e-05; tive 42; Mismatches 120; Indels
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; LOCATION: (1)..(212)
; OTHER INFORMATION: Ceres Seq.
US-11-096-568A-6282
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US-11-096-568A-6282
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Sequence-Determined DNA TITLE OF INVENTION: Therby FILE REFERENCE: 2750-1529US2 CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT FILING DATE: 2005-04-01 NUMBER OF SEQ ID NOS: 34471 SEQ ID NO 6282 LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6282, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                           112
169
                                     274 LAAGNSLEEACFFANAAAGVVVGKLGTSTVSP 305
                                                                                                             217 MKLIADYELSA--LLVTRSEQGMSLLQPGKAPLHMPT-QAQEVYDVTGAGDTVIGVLAAT 273
                                                                                                                                                                                       162 QMIQLARKAGVPVLIDPKGTDF----ERYRGATLLTPNLSEFEAVVG-KCKTEEEIVERG
                                                                                                                                                   52 QVAQAAKNAGVPVVLDAGGMDGPLPPQLINFVDILSPNETELARLTGMPTESFEEIQQAA 111
                                                                                                                                                                                                                               51;
                                                                       LKC---HEMGAKOVLVKLGHKGSALFVEGEKTIQQPAILAKTVVDTTGAGDTFTAAFAVA 168
LVEGKSKKECLRFAAAAACLCVQVKGASPSMP
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Pred. No. 7.9e-05;
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Search completed: March 18, 2006, 06:21:47 Job time : 25 secs

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Maximum Match 100%
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match
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1: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*
2: /cgn2 6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2 6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2 6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2 6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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-282-122A-60277
-282-122A-73168
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·335-977-5563
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815-242-13759
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71-241-325
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CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 469
LENGTH: 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Forsyth, R. Allyn
APPLICANT: Obleen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for
TITLE OF INVENTION: proliferation of E. coli
FILE REFERENCE: ELITEA.009A
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PastSEQ for Windows Version 4.0

3 US-09-815-242-11854	4 US-10-369-493-13944 S	4 US-10-369-493-17260	4 US-10-424-599-175504	5 US-10-501-282-3562	5 US-10-501-282-3560	4 US-10-369-493-16604		4 US-10-282-122A-50947	4 US-10-282-122A-65689	4 US-10-282-122A-65242	4 US-10-282-122A-49730	4 US-10-282-122A-48155	4 US-10-282-122A-50471	4 US-10-369-493-10214	4 US-10-369-493-37	4 US-10-282-122A-50163	4 US-10-282-122A-47619
Sequence 11854	Sequence 13944,	Sequence 17260	Sequence 17550	Sequence 3562,	Sequence 3560, Ap	Sequence 16604, A	Sequence 62085	Sequence 50947	Sequence 65689	Sequence 65242, A	Sequence 49730	Sequence 48155	Sequence 50471	Sequence 10214	Sequence 37, A	Sequence 50163	Sequence 47619

ALIGNMENTS

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301 STVSPIELENAVRGRADTGFGVMTEBELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 		181 TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL 241 OPGKAPLHMPTOAOEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT	121 FEEGFEGVDÞQÞLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 181 TDFERYRGATLLTPNLSEFEAVVGKCKTEBEIVERGMKLIADYELSALLVTRSEQGMSLL	121 FEEGFEGVDPQPLHERTINQALSSTGALVLSDYAKGALASVQQMTQLARKAGVPVLTDFKG	61 ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD	61 ASIGANARLVGLTGIDDAARALSKSLADVNVKCDEVSVPTHPTITKLRVLSRNQQLIRLD	1 MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPBAPVPVVKVNTIEERPGGAANVAMNI	1 MKVTLPEFERAGVAVVGDVALDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVÄMNI	Query Match 100.0%; Score 2393; DB 3; Length 477; Best Local Similarity 100.0%; Pred. No. 1.3e-198; Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps	; TYPB: PRT ; ORGANISM: Escherichia coli US-09-741-669-469
360	300	300	180 240	180	120	120	60	60	0.	

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APPLICANT: Trawick, John
APPLICANT: Forsyth, R. Allyn
APPLICANT: Forsyth, R. Allyn
APPLICANT: Froelich, Jamie M.
APPLICANT: Erroelich, Jamie M.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANTION: GENES IDENTIFIED AS REQUIRED FOR PROLIPERATION IN
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001DV1
CURRENT APPLICATION NUMBER: US/09/912,020
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR PILING DATE: 2000-01-27
PRIOR PILING DATE: 2000-01-27
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US-09-912-020-325
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PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 325
LENGTH: 477
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ORGANISM: E. (
S-09-912-020-325
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Best Local
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APPLICANT: Ohleen, Kari L.
APPLICANT: Trawick, John
APPLICANT: Forsyth, R. All:
APPLICANT: Froelich, Jamie
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US20020045592A1
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                                                                                  ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
                                                                                                                              STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 360
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IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDKKG
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RESULT 3
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CURRENT APPLICATION NUMBER: US/09/815,24:
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
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Best Local Similarity
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APPLICANT: Xu, H. Howard

IITLE OF INVENTION: Identification of Essential Genes

TITLE OF INVENTION: Prokaryotes
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ANARKLGDRLI VAVNSDASTKRLKGDSRPVNPLEQRMI VLGALBAVDWVVSFEEDTPQRL
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LENGTH: 477
TYPE: PRT
ORGANISM: Escherichia
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential
FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-02
CURRENT FILING DATE: 2003-02-02
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PRIOR FILING DATE: 2000-03-21
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/230,335
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FILING DATE: 2000-11-27
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APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
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                                                                                                              ASLGANARLYGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRYLSRNQQLIRLD
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Zyskind, Judith
Wall, Daniel
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Yamamoto, Robert
Forsyth, R.
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Malone, Cheryl
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100.0%; Pred. No. 1.3e-198;
tive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 325
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Best Local Similarity
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FILE REFERENCE: ELITHA.001C1
CURRENT APPLICATION NUMBER: US/10/771,241
CURRENT FILING DATE: 2004-02-03
FRIOR APPLICATION NUMBER: 09/492,709
FRIOR PILING DATE: 2000-01-27
PRIOR PILING DATE: 2000-01-27
PRIOR PILING DATE: 1099-01-27
PRIOR PILING DATE: 1099-01-27
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b. US20040241715A1
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100.0%; Pred. No. 1.3e-198;
tive 0; Mismatches 0;
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181 TDFERYRGATLLTPNLSEFEAVVGKCKTEEBIVERGMKLIADYELSALLVTRSEQGMSLL
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IAGILPDLLVKGGDYKPEBIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDKKG 477
                                                                                 ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
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FOR PROLIFERATION

Length Indels

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SOFTWARE: PatentIn version 3.1
SEQ ID NO 56202
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                                                                                                                                                                                                                                                       LENGTH: 476
TYPE: PRT
ORGANISM: Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT:
                                                                                                                                                                   y Match 95.9%; Score 2294; DB 4; Length 476;
Local Similarity 94.7%; Pred. No. 5.1e-190;
hes 451; Conservative 19; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
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FILING DATE: 2000-03-21
APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09 APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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 121
                                   61
                                                                 61 ASIGANARIVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
                                                                                                                                   1 MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI 60
FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 180
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                                                                                                     MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAFVFVVKVDTIEERFGGAANVAMNI
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Yamamoto, Robert
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Malone, Cheryl
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Trawick, John
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APPLICANT: Ohlsen, Ka:
APPLICANT: Zyskind, JI
APPLICANT: Wall, Danie
                                                                                                       Matches
                                                                                                                                     Query Match
                                                                                                                                                                         ORGANISM: Salmonella typhi
-09-815-242-13759
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                                                                                                   Local Similarity
les 445; Conserv
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ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto, Robert T.
Xu, H. Howard
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Zyskind, Judith W.
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                                                                                                       Conservative
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US-09-815-242-13759
; Sequence 13759, Application US/09815242
; Patent No. US20020061569A1
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 13759
LENGTH: 477
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/257,931
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MKVNLPAFERAGVMVVGDVMLDRYWYGPTCRISPEAPVPVVKVNTVEERPGGAANVAMNI
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                                                                                                       94.7%; Score 2265; DB 3;
93.5%; Pred. No. 1.7e-187;
bive 19; Mismatches 12;
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                                                                                                                                                         Length 477;
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RESULT 8
US-10-282-122A-75478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
    Remaining Prior
NUMBER OF SEQ II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                     OR PELICATION NUMBER: 60/230,347
OR FILING DATE: 2000-09-09
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-12-22
OR APPLICATION NUMBER: 60/267,636
OR RILING DATE: 2001-02-09
OR APPLICATION NUMBER: 60/269,308
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APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
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FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
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Zyskind, Judith
Wall, Daniel
Trawick, John
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Malone, Cheryl
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Application data removed NOS: 78614
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; ORGANISM: Salmonella typhi
US-10-282-122A-75478
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                 IAGILPDLLVKGGDYKPEBIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDKK 476
                                                                                 ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
                                                                                                                                          STVSPIBLENAVRGRADTGFGVMTEBBLKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
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IAGILPDLLVKGGDYKPEBIAGSEEVMANGGEVMVLNFEDGCST
                                                             ANARKLGDRLIVAVNSDASTKRLKGESRPVNPLEQRMIVLGALESVDWVVSFEEDTPQRL
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Pred. No. 1.7e-187;
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Sequence 60277, Application US/10282122A Publication No. US20040029129A1 APPLICANT: -10-282-122A-60277 APPLICANT: PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23 FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20 APPLICANT: PPLICANT: TLE OF INVENTION: Identification of Essential Genes in Microorganisms APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26 APPLICATION NUMBER: 60/230,335 FILING DATE: Wang, Liangsu
Zamudio, Carlos
Zamudio, Cheryl
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John Trawiu... Carr, Grant Carr, Grant Forsyth, R. NUMBER: 60/230,347 2000-09-06

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; TYPE: PRT
; ORGANISM: Klebsiella
US-10-282-122A-60277
APPLICANT: Wang, I
APPLICANT: Zamudi
APPLICANT: Malone
APPLICANT: Haselh
APPLICANT: Zyskin
APPLICANT: Wall,
APPLICANT: Trawic
APPLICANT: Trawic
APPLICANT: Yamamo
APPLICANT: Yamamo
APPLICANT: Forsyty
APPLICANT: Xu, H.
                                                                                                                                                                                    Sequence 73168, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 786.4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60277
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OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-12-22
OR APPLICATION NUMBER: 60/267,636
OR FILING DATE: 2001-02-09
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-16
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                                                                           Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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 Yamamoto, Ro
Forsyth, R.
Xu, H.
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                                                              Wall, Daniel
Trawick, John
                                              Carr, Grant
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lio, Carlos
                                 Robert
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Pred. No. 3.3e-184;
25; Mismatches 12;

    See File Wrapper or PALM

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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 73168
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Best Local :
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OR FILLING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR FILLING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILLING DATE: 2000-12-22
OR APPLICATION NUMBER: 60/267,636
OR APPLICATION NUMBER: 60/267,636
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-06
OR FILING DATE: 2001-02-16
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                 LLVKGGDYKPEBIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQ
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                                                                                         DRLIVAVNSDASTKRLKGDSRÞVNÞLEQRMIVLGALEAVDWVVSFEEDTÞQRLIAGILÞÓ
                                                                                                                                                                        LENAVRGRADTGFGVMTEBELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYLANARKJG
                                                                                                                                                                                                                            HMPTQAQEVYDVTGAGDTVIGVLAATLAAGNTLEEACYFANAAAGVVVGKLGTSTVSFIE
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LLVKGGDYKPEBIAGSEEVWPTGGEVMVLNFEDGCSTTNIIKKIQ
                                                                       DRLIVAVNSDASTKRLKGESRPVNPLEQRMIVLGALESVDWIVSFEEDTPQRLIAGILPD
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RESULT 11 US-10-282-122A-78165 ; Sequence 78165, Application

US/10282122A

Publication No. US20040029129A1

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SEQ ID NO 78165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Yersinia pestis
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Local Similarity 86.1%;
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FILING DATE: 2000-09-06
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APPLICATION NUMBER: 60/207,727
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APPLICATION NUMBER: 60/269,308
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STVSPIELENAVRGRADTGFGVMTBEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
                                                       QLGKPPLHLPTQAKEVFDVTGAGDTVTGVLAAALAAGNSLEESCFLANAAAGVVVGKLGT
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Zyskind, Judith
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Pred. No. 4.2e-171;
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US-10-282-122A-68720
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Publication No. US20040029129A1
                                                                                                                                          Matches 389;
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CURRENT FILING DATE: 2003-02-20
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PRIOR FILING DATE: 2000-03-21
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APPLICATION NUMBER: 60/207,727
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Zyskind, Judith
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Malone, Cheryl
Haselbeck, Robert
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moto, Robert
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              Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58533
LENGTH: 476
TYPE: PRT
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APPLICANT: Zamud
APPLICANT: Malon
APPLICANT: Hasel)
APPLICANT: Ohlse
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
ORGANISM: Haemophilus influenzae
                                                                                                                               OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-12-22
OR APPLICATION NUMBER: 60/267,636
OR APPLICATION NUMBER: 60/269,308
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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Wall, Daniel
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APPLICANT: FOREYTH, R.

APPLICANT: XU, H.

APPLICANT: XU, H.

APPLICANT: XU, H.

FITTLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: ELITEA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/203,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

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US-10-282-122A-67124
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APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Wang, Liangsu
: Zamudio, Carlos
: Malone, Cheryl
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Carr, Grant
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Forsyth, R.
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Zyskind, Judith
Wall, Daniel
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Pred. No. 1.6e-139;
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RESULT 15
US-10-282-122A-69312
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                                                                    APPLICANT:
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10-282-122A-67124
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hes 327; Conserv
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OR FILING DATE: 2000-12-22
OR APPLICATION NUMBER: 60/267,636
OR FILING DATE: 2001-02-09
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-16
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? INVENTION: Identification of Essential Genes in Microorganisms
PERENCE: ELITRA.034A
APPLICATION NUMBER: US/10/282,122A
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                                                                                                                                                         Wall, Daniel
Trawick, John
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Zyskind, Judith
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Malone, Cheryl
                                                                                                                                    Carr, Grant
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Forsyth, R.
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 69312
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Best Local
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-10-282-122A-69312
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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OR APPLICATION NUMBER: 60/242,578
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OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
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                                                                                                                                   AAISAPELRRAIQREEGSERGVLGLEQLLLAVDDARAHKEKIVFTNGCFDILHAGHVTYL
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Sequence 276, App Sequence 6204, App Sequence 6204, App Sequence 165, App Sequence 20018, App Sequence 20018, A Sequence 24093, A Sequence 35984, A Sequence 32536, A Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 30940, A Sequence 1, Appli Sequence 30940, A Sequence 7685, App Sequence 7681, Ap Sequence 7682, Ap Seq
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181 GCTTCTCTGGTGCTAATGCACGCCTGGTTCGGGTTGACGGGCATTGACGATGCACCCCC 24	181 GCTTCTCTCGGTGCTAATGCACGCCTGGTCGGGTTGACGGGCATTGACGATGCAGCGCC 24	121 GTTAAAGTGAATACCATCGAAGAACGTCCGGGGGGGGGG	121 GTTAAAGTGAATACCATCGAAGAACGTCCGGGCGGCGGCGGCGTAACGTGGCGATGAATATC 18	61 CTGGATCGTTACTGGTACGGCCCCACCAGTCGTATCTCGCCGGAAGCGCCGGTGCCCGTG 12	61 CTGGATCGTTACTGGTACGGCCCCACCAGTCGTATCTCGCCGGAAGCGCCGGTGCCCGTG 12	1 ATGAAAGTAACGCTGCCAGAGTTTGAACGTGCAGGAGTGATGGTGGTTGGT	1 ATGAAAGTAACGCTGCCAGAGTTTTGAACGTGCAGGAGTGATGGTTGGT	thes 1434; Conservative 0; Mismatches 0; Indels 0; Gaps	Tocal cimilarity 100.0%; Score	; LOCATION: (1)(1434) US-09-741-669-276	CDS	ORGANISM: Escherichia coli	TYPE: DNA	276	FastSEQ for	PILING I	APPLICATION NUMB	CURRENT APPLICATION NUMBER: US/09/741,669	BRENCE: ELITRA. 0091	TITLE OF INVENTION: genes identitied as required for	CANT: Zyskind, Judith W.	Ohlsen, Kari	APPLICANT: Forsyth, R. Allyn	INT INFORMATION:	ence 276, Application US/09741669	US-09-741-669-276	

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APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Yun H. Howard

TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN

TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN

TITLE OF INVENTION: ESCHERICHIA COLI

FILE REFERENCE: ELITRA, 001DV1

CURRENT APPLICATION NUMBER: US/09/912,020

CURRENT FILING DATE: 2001-07-23

PRIOR APPLICATION NUMBER: 09/492,709

PRIOR FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: 60/117,405

PRIOR APPLICATION DATE: 1999-01-27

NUMBER OF SEQ ID NOS: 485

SOPTWARE: FRASTSEQ for Windows Version 3.0

SEQ ID NO 165

LENGTH: 1434
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US-09-912-020-165
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Trawick, John
APPLICANT: Forsyth, R. Allyn
APPLICANT: Froelich, Jamie M.
APPLICANT: Carr, Grant J.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu, H. Howard
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Best Local Similarity
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Patent No.
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RESULT 3
US-09-815-242-6204
Sequence 6204, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
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US-09-815-242-6204
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION UNMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
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Best Local Similarity 100.0%;
Matches 1434; Conservative 0;
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 6204
LENGTH: 1434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-02-16
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ORGANISM: Escherichia coli
FEATURE:
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APPLICATION NUMBER: 60/269,308
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Xu, H. Howard
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                                                                               Sequence 6430, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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PRIOR FILING DATE: 2000-05-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-08
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
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Best Local Similarity
Matches 1434; Conserv
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ORGANISM: Escherichia
:-10-282-122A-6430
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Identification of Essential Genes
TILE REFERENCE: ELITEA.034A
CURRENT ENTION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
CURRENT FILING DATE: 2003-02-20
REIOR APPLICATION NUMBER: 60/191,078
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
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RESULT 5
US-10-771-241-165
/ Sequence 165, Application US/10771241
/ Publication No. US20040241715A1
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APPLICANT: FORSYth, R. Allyn
APPLICANT: FORSYth, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA,001C1
CURRENT APPLICATION NUMBER: U$/10/771,241
CURRENT FILING DATE: 2004-02-03
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
INUMBER: OF SEQ ID NOS: 485
SOPTMARE: FESTESEQ for Windows Version 3.0
SEQ ID NO 165
LENGTH: 1434
TYPE: DNA
ORGANISM: E. Coli
US-10-771-241-165
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        CAACCGGGTAAAGCGCCGCTGCATATGCCCAACCCCAAGCGCAGGAAGTGTATGACGTTACC 780
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Sequence 20018, Application US/10282122A

| Publication No. US20040029129A1
| GENERAL INFORMATION:
| APPLICANT: Wang, Liangsu
| APPLICANT: Wang, Liangsu
| APPLICANT: Haselbeck, Robert
| APPLICANT: Haselbeck, Robert
| APPLICANT: Wall, Judith
| APPLICANT: Wall, Daniel
| APPLICANT: Wall, John
| APPLICANT: Yamamoto, Robert
| APPLICANT: Yamamoto, Yamamoto, Robert
| APPLICANT: Yamamoto, Robert
| APPLICANT: Yamamoto, Yamamoto, Yamamoto, Yamamoto, Yamamoto, Robert
| APPLICANT: Yamamoto, Ya
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US-10-282-122A-20018
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PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: 60/230,335
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PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2010-12-22
PRIOR PRIOR PILING DATE: 2010-12-26
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2011-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2011-02-16
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NUMBER OF SEQ ID NOS: 786.4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20018
LENGTH: 1428
TYPE: DNA
ORGANISM: Enterobacter cloacae
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Yekind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential General Commence of INVENTION: Trokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION DATE: 2000-03-21
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GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/243,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-25
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2000-12-26
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOPTWARE: PASICSEQ FOR WINDOWS Version 4.
SEQ ID NO 9661
LENGTH: 1434
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Best Local Similarity
Matches 1164; Conserv
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ORGANISM: Salmonella typhi
FEATURE:
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LOCATION: (1)...(1434)
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    GCCGATTACGAACTCTCCGCTCTGTTAGTGACCCGTTCCGAACAGGGTATGTCGCTGCTG
                                                                                       GCTGTTGTCGGTAAATGTAAGACCGAAGAAGAGATTGTTGAGCGCGGCATGAAACTGATT
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81.8%; Pred. No. 0;
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Length 1434;

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APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
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US-10-282-122A-39294
                                                                                                                                                                                                                                                                                                                                                         Sequence 39294, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
APPLICATION NUMBER: 60/191,078
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SOFTWARE: Patentin version 3.1
SEQ ID NO 39294
LENGTH: 1434
TYPE: DNA
ORGANISM: Salmonella typhi
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Matches 1164;
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RR APPLICATION NUMBER: 60/257,931

DR FILING DATE: 2000-12-22

DR PILING DATE: 2000-12-05

DR FILING DATE: 2001-02-09

RR APPLICATION NUMBER: 60/269,308
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APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
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APPLICATION NUMBER: 60/253,625
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APPLICATION 1
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                     Sequence 24093, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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Yamamoto, Ru
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Xu, H.
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Trawick, John
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; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24093
; ENOTH: 1431
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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APPLICATION NUMBER: 60/230,347
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APPLICATION NUMBER: 60/242,578
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APPLICATION NUMBER: 60/230,335
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TITLE OF INVENTION: Identification of Essential Genes
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GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                RESULT 10
US-10-282-122A-36984
                                                                                                                                        Sequence 36984, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36984
LENGTH: 1397
TYPE: DNA
ORGANISM: Salmonella paratyphi A
US-10-282-122A-36984
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
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PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/243,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
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Best Local
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APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yangmoto, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential
FILE REPERENCE: ELITRA.034A
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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RESULT 11
US-10-282-122A-41981
Sequence 41981, Application US/10282122A publication No. US20040029129A1 GENERAL INFORMATION: APPLICANT: Wang, Liangsu APPLICANT: Zamudio, Carlos
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Remaining Prior Application data removed in NUMBER OF SEQ ID NOS: 78614

SOFTWARE: Patentin version 3.1

SEQ ID NO 41981

LENGTH: 1431

TYPE: DNA

ORGANISM: Yersinia pestis

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PRIOR PILLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILLING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILLING DATE: 2000-10-23
PRIOR PILLING DATE: 2000-11-27
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PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR APPLICATION NUMBER: 60/267,636
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APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Lianggu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Best Local
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
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Yamamoto, Robert
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RESULT 12 US-10-282-122A-32536

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PRIOR FILING DATE: 2000-03-21
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-29
PRIOR PILING DATE: 2000-12-67
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NUMBER OF SEQ ID NOS: 78614
SOPTWARE: PatentIn version 3.1
SEQ ID NO 32536
LENGTH: 1422
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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Pred. No. 2.1e-228;
0; Mismatches 435;
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; Remaining Prior Application data removed -
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22349
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
US-10-282-122A-22349
                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILLING DATE: 2000-03-21
PRIOR PILLING DATE: 2000-03-21
PRIOR PILLING DATE: 2000-05-23
PRIOR PILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILLING DATE: 2000-09-09
PRIOR PILLING DATE: 2000-09-09
PRIOR PILLING DATE: 2000-10-23
PRIOR PILLING DATE: 2000-11-27
PRIOR PILLING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILLING DATE: 2000-12-27
PRIOR PILLING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILLING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 60/269,306
PRIOR PILLING DATE: 2001-02-16
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; Sequence 22349, Application US/10282122A
; Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1381 GGTATTTCCACAACTAATATTATTAATGCCATTAAAAAGAA 1421
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
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Carr, Grant
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Zyskind, Judith
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TCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGACGGTTGCTCGACGACCA 1396
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                                                                                                                                                                                                                                                                                               ATTCCCGCCCGGTAAACCCACTCGAACAGCGTATGATTGTGCTGGGCGCACTGGAAGCGG 1216
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CURRENT APPLICATION NUMBER: US/10/329,670
CURRENT FILING DATE: 2002-12-24
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2000-08-23
PRIOR PILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR PILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOPTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1830121
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US-10-329-670-1/c
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TITLE OF INVENTION: Nucleotide Sequence of the
TITLE OF INVENTION: Thereof, and Uses Thereof
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NAME/KEY: misc feature
'COLTION: (36636)..(36636)
'COLTION: n equal
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (4747)...(4747)
OTHER INFORMATION: n equals
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LOCATION: (29298) . (29298)
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LOCATION: (9921)..(9921)
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LOCATION: (44905)...(44905)
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LOCATION: (44416)..(44416)
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LOCATION: (40808)..(40810)
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LOCATION: (119750)..(119750)
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LOCATION: (117136)..(117136)
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LOCATION: (107248)..(107248)
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OCATION: (102696)..(102696)
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)CATION: (80024)..(80024)
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OCATION: (65313)..(65313)
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)CATION: (65309)..(65309)
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OCATION: (51786)..(51786)
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OCATION: (51602)..(51
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LOCATION: (150841)..(150841)
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LOCATION: (147197)..(147197)
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LOCATION: (145942)..(145942)
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LOCATION: (121344)..(121344)
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NAME/KEY: misc_feature
LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals
                                                NAME/KEY: misc_feature
LOCATION: (152530)..(152530)
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LOCATION: {145058}..(145058)
OTHER INFORMATION: n equals
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LOCATION: (142750)...(142750)
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LOCATION: (131340)..(131340)
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LOCATION: (122336)..(122336)
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LOCATION: (122167)..(122167)
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LOCATION: (145171)..(145171
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LOCATION: (140398)..(140398)
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                                                               TGGGCGATCGTCTAATTGTTGCGGTAAACAGCGACGATTCTGTTAAACGCTTAAAAGGTG
                                                                                                                                                                                             ATGGCTGTTTTGATÄTTTTGCÄTCCAGGGCÄTATTTCTTATTTAGAÄÄÄTGCACGCÄÄAAT 1595475
                                                                                                                                                                                                                                                      ACGGTGTCTTTGACATCCTGCACGCCGGGCACGTCTCTTATCTGGCAAATGCCCGCAAGC 1096
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                                                                                                                       TGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCCTCCACCAAACGGCTGAAAGGGG 1156
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Sequence 1, Application US/10158865

Publication No. US20040203093A1

GENERAL INFORMATION:

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd G

TITLE OF INVENTION: Thereof, and Uses Thereof

FILE REFERENCE: PB186P2CLD1

CURRENT APPLICATION NUMBER: US/10/158,865

CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: US 09/557,884

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: US 08/476,102

PRIOR APPLICATION NUMBER: US 08/476,102

PRIOR FILING DATE: 1995-04-21

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 1830121
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LOCATION: (10150)..(10150)
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misc_feature
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PARTURE: NAME/KEY: misc festure LOCATION: (107248)(107248)	NAME/KEY: misc feature LOCATION: (105121)(105121) OTHER INFORMATION: n equals a,t,c, or g	NAME/KEY: misc feature LOCATION: (102696)(102696) OTHER INFORMATION: n equals a,t,c, or g	NAME/KEY: misc feature LOCATION: (100091)(100091) OTHER INFORMATION: n equals a,t,c, or g FRATURE:	NAME/KEY: misc feature LOCATION: (80024)(80024) OTHER INFORMATION: n equals a,t,c, or g	NAME/KEY: misc feature LOCATION: (65313)(65313) OCTHER INFORMATION: n equals a,t,c, or g	NAME/KEY: misc feature LOCATION: (65309)(65309) OTHER INFORMATION: n equals a,t,c, or g	NAME/KEY: misc feature LOCATION: (55369)(55369) OTHER INFORMATION: n equals a,t,c, or g	NAME/KEY: misc feature LOCATION: (51805)(51805) OTHER INFORMATION: n equals a,t,c, or g	NAME/KEY: misc feature LOCATION: (51786)(51786) OTHER INFORMATION: n equals a,t,c, or g	NAME/KEY: misc feature LOCATION: (51602)(51602) OTHER INPORMATION: n equals a,t,c, or g	PARLUE: misc feature LOCATION: (51334)(51334) OTHER INFORMATION: n equals a,t,c, or g FRATURE:	NAME/KEY: misc feature LOCATION: (47036)(47036) OTHER INFORMATION: n equals a,t,c, or g	NAME/KEY: misc feature LOCATION: (45732)(45732) OTHER INFORMATION: n equals a,t,c, or g	NAME/KEY: misc feature LOCATION: (45593)(45593) OTHER INFORMATION: n equals a,t,c, or g	NAME/KBY: misc feature LOCATION: (44975)(44975) OTHER INFORMATION: n equals a,t,c, or g	NAME/KEY: misc feature LOCATION: (44905)(44905) OTHER INFORMATION: n equals a,t,c, or g FRATURE:		LOCATION: (40808)(40810) OTHER INFORMATION: n equals a,t,c, or g FEATURE:
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LOCATION: (119924)..(119924)
OTHER_INFORMATION: n equals
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LOCATION: (119750)..(119750)
OTHER_INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (145171)..(145171)
OTHER_INFORMATION: n equals a,t,c,
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (122336)..(122336)
OTHER_INFORMATION: n equals a,t,c,
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LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (140398)..(140398)
DTHER_INFORMATION: n equals a,t,c,
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LOCATION: (131360)..(131360)
WITHER INFORMATION: n equals
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.OCATION: (131340)...(131340)
THER INFORMATION: n equals a,t,c,
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	ACCGAAG 976		917	Ş
	TCGACCG 1595655	TAGCCAATGTTGCCGCAGGAATTGTGGTGGGGAAATTGGGGACTTCAACGGTTTCGACCG	1595714	밁
	TCGCCGA 916	TTGCCAATGCGGCGGCTGGCGTGGTGGTCGGCAAACTGGGAACCTCCACGGTT	857	S
	IGCTICE 856	TCATTAGCGTATTAGCAACCGCATTAGCAGATGGACGTTCTTTCGAAGAATCTTGTTACC	1595774	ß 8
	ן נ	CTTATCATTTGCCAACTGTTGCAAAAGAGTGTTTGATGTGACGGGAGCCGGT	1595834	}
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	GAGCGCT 556 GAACGTT 1596015	TGGCGCGTAAAGCGGGTGTTCCGGTGCTGATTGATCCAAAAGGTACCGATTTTGAGCGCT	497 1596074	ß 5
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	ATTGGCG 436 	AAGGTGTTGATCCGCAGCCGCTGCACCGAGCGGATTAATCAGGCGCTGAGTTCGATTGGCG	377 1596194	유 성
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	GTTTCG 376		317	ફ
	ATTACCA 316 ATTACTA 1596255	TGGCCGACGTCAACGTCAAATGCGACTTCGTTTCTGTACCGACGCATCCGACCATTACCA	257 1596314	용 <i>各</i>
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	21; Gaps 0;	ch 44.3%; Score 635.2; DB 8; Length 183012 1 Similarity 65.9%; Pred. No. 2.9e-197; 922; Conservative 0; Mismatches 478; Indels 0;	Query Match Best Local : Matches 92:	7 M O
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1396	1337 TCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGACGGTTGCTCGACGACCA	Ş
1595235	1595294 CAGATCTTTTAGTCAAAGGCGGCGATTACAAACCCGAAGAATTGCAGGCAG	В
1336	1277 CAGATCTGCTGGTGAAAGGCGGGGACTATAAACCAGAAGAGATTGCCGGGAGTAAAGAAG	Ş
1595295	1595354 TAGACTGGTTGGTGCCTTTCACTGAAGATACACCACAACGTTTAATCGGCGAAATTCTAC	뭣
1276	1217 TCGACTGGGTAGTGTCGTTTGAAGAGGGACACGCCGCAGCGCTTGATCGCCGGGATCTTGC	ঠ
1595355	1595414 AAAGTCGCCCAATTAATATTCTTGAAAAACCGTATGGCGGTATTGGCTGGTTTGGCATCCG	뭣
1216	1157 ATTCCCGCCCGGTAAACCCACTCGAACAGCGTATGATTGTGCTGGGCGCACTGGAAGCGG	ঠ
1595415	1595474 TGGGCGATCGTCTAATTGTTGCGGTAAACAGCGACGATTCTGTTAAAACGCTTAAAAGGTG	당
1156	1097 TGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCCTCCACCAAACGGCTGAAAGGGG	8
1595475	1595534 ATGCTGTTTTGATATTTTGCATCCAGGCATATTTCTTATTTAGAAAATGCACGCAAAT	닭
1096	1037 ACGGTGTCTTTGACATCCTGCACGCCGGGCACGTCTCTTATCTGGCAAATGCCCGCAAGC	ঠ
1595535	1595594 CAGAATTAAAAGATGCTGTCGCACAAGCTAAAGCGCGCGGTGAAAAAATTGTGATGACTA	dd

Search completed: March 19, 2006, 13:26:17 Job time: 2103 secs

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ALIGNMENTS

RESULT 1 AAA65973 03-AUG-2000 Escherichia coli. Escherichia coli; E. coli; proliferation; inhibition; screening; antimicrobial; bacterial growth; antisense therapy; antibacterial; ds. E. coli proliferation associated coding sequence SEQ ID NO:165. 05-OCT-2000 (first entry) AAA65973; AAA65973 standard; DNA; 1434 BP 27-JAN-2000; 2000WO-US002200 WO200044906-A2.

27-JAN-1999; 99US-0117405P

(BLIT-) BLITRA PHARM INC.

Zyskind J, Ohlsen KL, Carr GJ, Yamamoto RT, Trawick J, Xu HH; Forsyth RA, Froelich JM;

WPI; 2000-514822/46. P-PSDB; AAB15968.

Novel polynucleotides and polypeptides associated with microorganism proliferation, used to identify inhibitors of bacterial growth and proliferation, for use in antisense therapy.

Claim 8; Page 146-147; 316pp; English.

AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide sequences derived from Escherichia coli which inhibit E. coli proliferation. AAA65890 to AAB168055 and AAB15886 to AAB16040 represe nucleotide and protein sequences associated with E. coli proliferation. E. coli proliferation.

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26-MAY-2000; 2000US-027727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-025362SP.
22-DEC-2000; 2000US-025931P.
16-FEB-2001; 2001US-0269308P.
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Haselbeck R, Yamamoto RT,

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CC The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes could be used to the encoded proteins. The prokaryotes used are Bacherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coli, Staphylococcus and Enterococcus faecalis. The invention is also cuseful for the identification of potential new targets for antibiotic colored to the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent color format directly from WIPO at cellular intromb/mbhlished not served.
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TCGACG	AGTAAA AGTAAA	GGGATC	CTGGAA	CTGAAA CTGAAA	900000 	GIGATG	ATGACC	GITTOG GITTOG	ecciec	GGCGAC	GGTAAA	TACGAA	GICGGI GICGGI
ACCAAC	SAAGTCI	TIGCCAG	GCGGTCG	GGGATT	NAGCTIGG NAGCTIGG	ACCAACC	SAAGAGG SAAGAGG	CCGATCC		ACGGTGF	3060000 		NAATGTA NAATGTA
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GGTTGCTCGACGACCAACATCATCAAGAAGATCCAACAGGATAAAAAAGGCTAA 	GCCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGAC 	ATCGCCGGGATCTTGCCAGATCTGCTGGTGATAAAGGCGGCGACTATAAACCAGAAGAGATT 	GGCGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAGAGGACACGCCGCAGCGCTTG	AAACGGCTGAAAGGGGATTCCCGCCCGGTAAACCCACTCGAACAGCGTATGATTGTGCTG	GCAAATGCCCGCAAGCTGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCCTCCACC	AAAGTGGTGATGACCAACGGTGTCTTTGACATCCTGCACGCCGGGCACGTCTCTTATCTG 	GGCGTGATGACCGAAGAGGAACTGAAGCTGGCCGTAGCGGCAGCGCGTAAACGTGGTGAA 	TCCACGGTTTCGCCGATCGAGCTGGAAAATGCTGTACGTGGACGTGCAGATACAGGCTTT 	GAAGAAGCCTGCTTCTTTGCCAATGCGGCGGCTGGCGTGGTGGTGGTCGGCAAACTGGGAACC 	GGTGCGGGCACACGGTGATTGGCGTCCTGGCGGCAACGCTGGCAGCGGGTAATTCGCTG	CAACCGGGTAAAGCGCCGCTGCATATGCCAACCCAAGCGCAGGAAGTGTATGACGTTACC	GCCGATTACGAACTCTCGGCTCTGTTAGTGACCCGTTCCGAACAGGGTATGTCGCTGCTG	GCTGTTGTCGGTAAATGTAAGACCGAAGAAGAGATTGTTGAGCGCGGCATGAAACTGATT
CCAACA	GAAGT	NAGGCGG NAGGCGG	GTTTGA	ACCCACT	TGTTGC	CCTGCA	CGTAGC	TGTACG	TIGGCGT	GGCAAC GGCAAC	CCAAGC	CCGTTC	GATTGT
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AAH81477 standard; DNA; 1434 ВP

21-SEP-2001 (first entry)

Escherichia coli protein encoding nucleotide sequence SEQ ID NO:276

Escherichia coli, identification, proliferation, microorganism, antimicrobial, antibacterial, antibiotic, gene therapy, diagnosis, bacterial growth inhibition; ds.

Escherichia coli

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a purified or isolated nucleic acid CC sequence (I) consisting essentially of one of the 93 nucleotide sequences CC given in AAH81202 to AAH81294, where expression of the nucleic acid in a CC microorganism is capable of inhibiting proliferation of a microorganism.

(I) have antibacterial and antibiotic activities, and can be used in gene CC the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that CC inhibit bacterial growth or proliferation can be used as antisense CC therapputics for killing bacteria. In addition to therapeutic acid sthat CC applications, the nucleic acid sequences complementary to sequences concluded for proliferation can be used as diagnostic tools. For example, nucleic acid probes complementary to proliferation required sequences that are specific for particular species of microorganisms can be used as concluded as diagnostic tools. For example, cc probes to ldentify particular species of microorganisms can be used as given in AAG98239 to AAG98431, and AAH81488 to AAH81491 represent colinocal colinocal which are used in the exemplification of the present colinocal colinocal which are used in the exemplification of the present colinocal colinocal which are used in the exemplification of the present colinocal colinocal which are used in the exemplification of the present colinocal invention.
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Best Local S
Matches 1434
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                                                                     GGTTGCTCGACGACCAACATCAACAAGAAGATCCAACAGGATAAAAAAGGCTAA 1434
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1260

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ACA18560 standard; DNA; 1434 BP.

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cc the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid concoling a polypeptide whose expression is inhibited by the antisense concoling a polypeptide whose expression is inhibited by the polypeptide or its fragment whose expression is inhibited by the cantisense concoling a polypeptide; (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated containing the polypeptide; (4) an isolated containing the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular containing the polypeptide; (7) identifying a compound that influences the activity of the polypeptide; (8) inhibiting cellular proliferation; (7) identifying a gene in an operon required for containing an activity against a biological pathway in which a proliferation, or that inhibits proliferation or the biological pathway in which a proliferation required for cellular proliferation or the biological pathway in which the test compound that inhibits proliferation of an companism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene contains; or (13) identifying the target of a compound that inhibits the gene contains; or (13) identifying the target of a compound that inhibits the condition of an organism. The antiense nucleic acids are useful for clanuflying proteins or screening for homologous nucleic acids required contains; or contains in which the contains in which the capacity of containing the capac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang L,
Wall D,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-PEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; SEQ ID NO 6430; 1766pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prokaryotic essential gene #217.
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Trawick JD,
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Carr GJ,
_pct_sequences
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Yamamoto R,
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Forsyth RA,
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Xu HH;
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Sequence 1434 BP; 328

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352 C; 447 G; 307

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                                                                              Identifying and selecting a gene required for the proliferation in vi of a pathogenic microorganism comprises determining the virulence of mutant genes on an experimental model of infection, and their effect enteric colonization.
                                         Claim 5; SEQ
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DB; ADH88979.
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infection; extra-intestinal infection; enterobacterium; g
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                                         ID NO 28;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene required for the proliferation in vivo of a pathogenic microorganism. The method comprises determining the virulence of mutant genes on an experimental model of infection, and their effect on enteric colonization in an axenic mouse model. ADH88967-ADH88991 and ADH89982-ADH88996 are pathogenicity or virulence targets and their coding sequences which were used in the method of the invention. Compounds capable of inhibiting pathogenicity or virulence target expression are useful for developing medicinal products for inhibiting a bacterial infection, in particular an extra-intestinal infection in the case of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1434 BP; 328 A; 352 C; 447 G; 307 T; 0 U; 0 Other;
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                                                                                                                         CAACCGGGTAAAGCGCCGCTGCATATGCCAACCCAAGCGCAGGAAGTGTATGACGTTACC
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                                                                                                                                                                                                                                                          GCTGTTGTCGGTAAATGTAAGACCGAAGAAGAGAATTGTTGAGCGCGGCATGAAACTGATT
                                                                                                                                                                                                                                                                                     GCTGTTGTCGGTAAATGTAAGACCGAAGAAGAAGATTGTTGAGCGCGGCATGAAACTGATT
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7ative 0; Mismatches
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-PEB-2002; 2002US-0362699P.
                                                                                                                                                                                                                                          Enterobacter cloacae
                                                                                                                                                                                                                                                                                Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                           21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                 WO200277183-A2
                                                                                                                                                                                                                                                                                                           Prokaryotic essential gene #13805
                                                                                                                                                                                                                                                                                                                                                                  ACA32148,
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           Zamudio C,
Trawick JD,
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           Malone C,
         Haselbeck R, Yamamoto R,
        Ohlsen I
Forsyth
         Zyskind JW;
Xu HH;
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WPI; 2003-029926/02

New antisense nucleic acids, useful for identifying proteins or a for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs or screening. 6

Claim 14; SEQ ID NO 20018; 1766pp; English

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression confirmation of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense culleic acid; (2) a host cell containing the vector; (3) an isolated continuous control of the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular culliferation or the activity of agene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation or proliferation, or that inhibits gene product lies or agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound to activity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the test of confideration of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required cor cellular proliferation in cells other than S. aureus, S. typhimurium, C. in the printed specification, but was obtained in the target core produced for the printed specification, but was obtained in celectoric format directly from WIPO at the curron of the compound that proliferation of the printed specification, but was obtained in .int/pub/published_pct_sequences

Sequence 1428 BP; 292 A; 388 C; 489 G; 259 T; 0 U; 0 Other;

Length 1428;

Query Match Best Local Similarity

밁 δ 밁 δ 밁 S S 밁 S 문 片 S Matches 1170; 361 301 301 241 241 181 181 121 121 61 61 GTTAAAGTGAATACCATCGAAGAACGTCCGGGCGGCGGCGGCTAACGTGGCGATGAATATC CTGGATCGTTACTGGTACGGCCCCACCAGTCGTATCTCGCCGGAAGCGCCCGGTGCCCGTG TTTGAAGAAGGTTTCGAAGGTGTTGATCCGCAGCCGCTGCACGAGCGGATTAATCAGGCG CACCCGACCATCACCAAGCTGCGCGTGCTGTCGCGCAACCAGCAGCTGATCCGCCTCGAC GCGCTGAGCAAGTCGCTGGCGGACGTGAACGTGAAGTGCGACTTCGTCTCTGTTCCGACC GCGCTGAGTAAATCTCTGGCCGACGTCAACGTCAAATGCGACTTCGTTTCTGTACCGACG GCCTCTCTGGGCGCGCAGTCGCGTCTGGTGGGCCTGACCGGCATCGACGATGCGGCGCGC GCTTCTCTCGGTGCTAATGCACGCCTGGTCGGGTTGACGGCATTGACGATGCAGCGCGC GTTAAGGTCGACACCATTGAAGAGCGTCCCGGCGGCGGCGAAACGTGGCGATGAACATT CTGGATCGCTATTGGTATGGGCCTACCAGCCGCATCTCTCCGGAAGCACCGGTACCGGTG ATGAAAGTAACACTGCCAGAGTTTGAACGTGCTGGGGGTAATGGTTGTTGGGGATGTGATG Conservative 71.0%; 82.2%; Score 1018.2; DB 8; Pred. No. 8.5e-292; 0; Mismatches 253; Indels <u>,</u> 360 300 300 240 240 180 180 120 120 60 60 0

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                       GGTTGCTCGACGACCAACATCATCAAGAAGATCCAACAGGATA 1423
                                                                                                        GCCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGAC
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GGGTGCTCAACCACCAACATCATCAAGAAGATCCAGAAGGACA 1423
                                                                                  GCGGGCAGCGAAGAGGTCTGGGCGAACGGCGAGGTGATGGTGCTCAACTTTGAGGAC
                                                                                                                                                                   ATTGCCGGCATTCTGCCGGACCTGCTGGTAAAAGGTGGGGATTACAAGCCGGAGCAAATC
                                                                                                                                                                                             ATCGCCGGGATCTTGCCAGATCTGCTGGTGAAAGGCGGCGACTATAAACCAGAAGAGATT
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This sequence encodes a Klebsiella pneumoniae of the invention
                                                                                                                                                                                                                                                                                                                                                                Sequence 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding a Klebsiella pneumoniae polypeptide, preparing a vaccine composition against Klebsiella pneumoniae.
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                                                         GCGCTGAGTAAATCTCTGGCCGACGTCAACGTCAAATGCGACTTCGTTTCTGTACCGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression vector; transcription regulatory element; pneumoniae protein; antibacterial; Vaccine; gene; ds
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                                      GGTTGCTCGACGACCAACATCATCAAGAAGATCCAACAGGATA 1423
                                                                                                                      GCCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGAC 1380
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RESULT 8 AAS56024

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Conservative

70.3**%**; 81.8**%**;

; Score 1008.6; ; Pred. No. 6.1e. 0; Mismatches

ed. No. 6.1e-289; Mismatches 259;

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Length 1434;

Query Match Best Local

Sequence 1434 BP; 311 A; 360 C; 468 G; 295 T; 0 U; 0 Other;

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The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the genes, cc their use in the discovery of novel antibiotics, the essential genes cc themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalls. The invention is also cu useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify cc proteins used in proliferation, to express these proteins, and to obtain can be used to screen compounds in rational drug discovery programmes. The can used to screen compounds in rational drug discovery programmes. The can used to acids which are required for cell proliferation in a wide variety cof organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent cc did not form part of the printed specification, but was obtained in the capture of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID NO 9661; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haselbeck R, Yamamoto RT,
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antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BLIT-) BLITRA PHARM INC
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; 2000US-0207727P.
; 2000US-0242578P.
; 2000US-0253625P.
; 2000US-0257931P.
; 2001US-0269308P.
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Xu HH;
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drug design.
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Claim 14;

SEQ ID NO 39294; 1766pp;

English.

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The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid complete acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense CC antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for CC the gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation; (8) CC required for proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an

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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or a for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs
                                                                                                                                                                                                                                                                                                                  21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                   03-OCT-2002.
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Xu HH;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1434 BP; 311 A; 360 C; 468 G; 295 T; 0 U;
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Antisense; ds; prokaryotic essential Prokaryotic essential gene design; gene.

gene; cell proliferation;

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-PEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107 03-OCT-2002. Klebsiella pneumoniae WO200277183-A2

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                                                                                                                                                                                                                                                                                                                                                                                     Matches 1163;
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cc polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular crowding the polypeptide; (6) inhibiting cellular crowding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which the test compound that inhibits proliferation of an corganism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent convolution of the strains; or (13) identifying the target of a compound that inhibits the gene convolution of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational convolutions of strains or screening for homologous nucleic acids required for cellular proliferation in cells other than S. sureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did cont form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                        the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operation 11 linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-PEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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06-SEP-2001; 2001US-00948993.

25-0CT-2001; 2001US-034923P.

08-FEB-2002; 2002US-00072851.
  Claim 14; SEQ ID NO 41981; 1766pp; English
                                     New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                            (ELIT-)
                                                                                                                                                                                                                                                                                   06-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002;
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DB; ABU50241.
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Trawick JD,
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The invention relates to an isolated nucleic acid comprising any one of control the fall antisense sequences given in the specification where expression of of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid control of a cell. Also included are: (2) a host cell containing the vector; (3) an isolated control of a cell. Also included are: (2) a host cell containing the vector; (3) an isolated control of antisense nucleic acid; (4) an antibody capable of specifically binding cellular producing the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway or identifying a gene required for cellular proliferation; (8) cidentifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound that inhibits proliferation of an organism, or (13) identifying the target of a compound that inhibits the compound that inhibits the extent contifying proteins or screening for homologous nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational contifying decembers and contifying the target of a compound that inhibits the control of an organism. The antisense nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, control of the printed specification, but was obtained in the target control of the printed specification, but was obtained in cells of the printed specification, but was obtained in cells of the carget control of the carget of the printed specification, but was obtained in cells of the carget carget carget carget carget carget car
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Sequence 1431 BP; 314 A; 325 C; 433 G; 359 T; 0 U; 0 Other;

Matches 1082; Query Match Best Local Similarity Conservative 61.3%; 76.2%; 0 Score 879.2; Pred. No. 1.9 Mismatches 1.9e-250; DB 8 Indels Length 1431; 0; Gaps

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TTTGAAGAAGGTTTTCGAAGGTGTTGATCCGCAGGCGGCTGCACGAGCGGATTAATCAGGCG
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                                                                       CTGAGTTCGATTGGCGCGCTGGTGCTTTCTGACTACGCCAAAGGTGCGCTGGCAAGCGTA
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RESULT 13
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Best Local Similarity 81.4
Matches 1005; Conservative
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1320 85244	1261 ATCGCCGGGATCTTGCCAGATCTGCTGGTGAAAGGGGGGGACTATAAACCAGAAGAGATT 1	_
1260 85304	1201 GGCGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAGAGGACACGCCGCAGCGCTTG 1	_
1200 85364	1141 AAACGGCTGAAAGGGGATTCCCGCCCGGTAAACCCACTCGAACAGCGTATGATTGTGTGCTG 1	_
1140 85424	1081 GCAAATGCCCGCAAGCTGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCCTCCACC 1	_
1080 85484	1021 AAAGTGGTGATGACCAACGGTGTCTTTGACATCCTGCACGCCGGGCACGTCTCTTATCTG 1	_
1020 85544	961 GGCGTGATGACCGAAGAGGAACTGAAGCTGGCCGTAGCGGCGGTAAACGTGGTGAA 1	_
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Search completed: March 18, 2006, 19:07:31 Job time : 945 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.

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2393
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Protein e	Protein e	N. gonorr	Protein e	Protein e	Protein e	Helicobac	Protein e	Bacterial	Helicobac	Bacterial	Protein e	Protein e	Protein e	Protein e	H. pylori	Protein e	N. gonorr	Protein e	Neisseria	Protein e	

ALIGNMENTS

RESULT 1
ARB15968
ID ARB15968
ID ARB1
XX ARB1
AX ARB1 27-JAN-1999; 03-AUG-2000. Escherichia coli. Escherichia coli; E. coli; proliferation; inhibition; screening; antimicrobial; bacterial growth; antisense therapy; antibacterial. E. coli proliferation associated protein sequence SEQ ID NO:325. 05-OCT-2000 AAB15968; AAB15968 standard; protein; 477 AA. 27-JAN-2000; 2000WO-US002200 WO200044906-A2 (BLIT-) BLITRA PHARM INC. (first entry) 99US-0117405P

Novel polymucleotides and polypeptides associated with microorganism proliferation, used to identify inhibitors of bacterial growth and proliferation, for use in antisense therapy.

Claim 11; Page 242-243; 316pp; English.

N-PSDB; AAA65973. WPI; 2000-514822/46. Zyskind J, Ohlsen KL, Carr GJ, Yamamoto RT,

Trawick J, Xu HH;

Forsyth RA, Froelich JM;

AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide sequences derived from Escherichia coli which inhibit E. coli proliferation. AAA65890 to AAA66055 and AAB15886 to AAA16040 represent nucleotide and protein sequences associated with E. coli proliferation. AAA66057 represent primers used for sequencing E. coli proliferation inhibiting nucleotide inserts in an example from the present invention can be used to identify a proliferation- required gene in a microorganism. By contacting identify a proliferation- required gene in a microorganism. By contacting the proliferation con activity inhibitory

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RESULT 2
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the genes. CC their use in the discovery of novel antibiotics, the essential genes CC themselves and the encoded proteins. The prokaryotes used are Escherichia CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, CC pseudomonas aeruginosa and Enterococcus faecalis. The invention is also CC useful for the identification of potential new targets for antibiotic CC development. The antisense nucleic acids can also be used to identify CC proteins used in proliferation, to express these proteins, and to obtain CC antibodies capable of binding to the expressed proteins, and to obtain CC antisense nucleic acids equence is also useful to screen for homologous CC antisense nucleic acids sequence is also useful to screen for homologous CC callular proliferation protein. Note: The sequence data for this patent CC cellular proliferation protein. Note: The sequence data for this patent CC did not form part of the printed specification, but was obtained in CC electronic format directly from WIPO at
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N-PSDB; AAS52567.
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                                                                                    ANARKLGDRLI VAVNSDASTKRLKGDSRPVNPLEQRMI VLGALEAVDWVVSFEEDTPQRL
                                                                                                                                                         STVSPIBLENA VRGRADTGFGVMTBEBLKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
                                                                                                                                                                                                    QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFPANAAAGVVVGKLGT
                                                                                                                                                                                                                     QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT
                                                                                                                                                                                                                                                                                            TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 AA;
                   IAGILPDLLVKGGDYKPEBIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDKKG 477
                                                                 ANARKI.GDRLIVAVNSDASTKRIKGDSRPVNPLEQRMIVI.GALEAVDWVVSFEEDTPQRL
                                                                                                                                  STVSPIELENAVRGRADTGFGVMTEBELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2393; DB 4;
Pred. No. 6.9e-207;
); Mismatches 0;
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RESULT 3 AAG98421 ID AAGS

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                                                                                                                                                                                                                                                                                                                                                        the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. In addition to therapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as diagnostic tools. For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. AAH81295 to AAH81487 encode the Escherichia coli proteins given in AAG8239 to AAG98431, and AAH81488 to AAH81491 represent properties of the present oliginal process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a purified or isolated nucleic acid sequence (I) consisting essentially of one of the 93 nucleotide sequences given in AAH81202 to AAH81294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism.

(I) have antibacterial and antibiotic activities, and can be used in gene therapy. Expression of (I) in a microorganism inhibits proliferation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids encoding proteins required for Escherichia proliferation, useful for screening for antimicrobial agents.
                                                                                                                                                                                                                                                                                                           Sequence
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Pred. No. 6.9e-207;
; Mismatches 0;
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                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or so
for homologous nucleic acids required for cellular proliferation t
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                             WPI; 2003-029926/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic essential gene; cell proliferation;
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Trawick JD,
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Forsyth
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Xu HH;
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the polypeptide cacid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of a gene in an operon required for

activity of

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Claim 25;

SEQ ID NO 42614; 1766pp; English.

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Matches 477
   Escherichia Synthetic.
                                                                                            Pathogenic microorganism; K1 S26; mutant; pathogenicity; virulence; bacterial infection; extra-intestinal infection; enterobacterium.
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Pred. No. 6.9e-207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for identifying and selecting a gene required for the proliferation in vivo of a pathogenic microorganism. The method comprises determining the virulence of mutant genes on an experimental model of infection, and their effect on enteric colonization in an axenic mouse model. ADH89967-ADH8991 and ADH8982-ADH88996 are pathogenicity or virulence targets and their coding sequences which were used in the method of the invention. Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             capable of inhibiting pathogenicity or virulence target expression are useful for developing medicinal products for inhibiting a bacterial infection, in particular an extra-intestinal infection in the case of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14;
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DB; ADH88994.
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                                                            ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
                                                                                                                       STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
                                                                                                                                                                QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT
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IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDKKG
                                       ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
                                                                                                    STVSPIELENAVRGRADTGFGVMTEBELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
                                                                                                                                                                                                                             TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              selecting a gene required for the pu
microorganism comprises determining
an experimental model of infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SA
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ng the virulence on, and their effec
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Gaps

IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDKKG

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360

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120 60 60 0

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RESULT 6
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                                                                                                                                                                                                                                                               cc nucleic acid; (2) a host cell containing the vector; (3) an isolated copyopetide or its fragment whose expression is inhibited by the cc antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits gene product lies or a gene on which the test compound that inhibits proliferation of an corganism acte; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of accides are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to repart or for screening homologous nucleic acids required constants. The antise security is acida.
                                                           drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or paralysinosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001U9-00815242.
06-SEP-2001; 2001U9-00948993.
25-OCT-2001; 2001U5-0342923P.
08-PEB-2002; 2002U5-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the nucleic acid inhibits proliferation of a cell. Also included are: ) a vector comprising a promoter operably linked to the nucleic acid
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Trawick JD,
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Carr GJ,
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26-MAY-2000;
23-OCT-2000;
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            Haselbeck R,
Yamamoto RT,
                                                                                                                                            21-MAR-2000; 2000US-0191078P
                                                                                                                                                                     21-MAR-2001; 2001WO-US009180
                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                          Salmonella typhi
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                                                                                                                                                                                                                                                                                                      Salmonella typhi cellular proliferation
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                                             BLITRA PHARM INC
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2001US-0269308P
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2000US-0207727P
2000US-0242578P
           Ohlsen KL,
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                      Zyskind JW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain a misodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent of the printed specification, but was obtained in
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Best Local S
Matches 445
 19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             did not form part of the printed specification, electronic format directly from WIPO at
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                                     ABU47554;
                                                                        ABU47554 standard; protein; 477
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93.5%;
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Pred. No. 2.5e-195;
19; Mismatches 12; Indels
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The invention relates to an isolated nucleic acid comprising any one of the fall antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of eell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense conclude acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense continued in the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene product or that has an activity against a biological pathway of required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which he test compound that inhibits gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound section of an organism acts; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational contraction and isovery programs or for acreening but and antisense molecules for rational contractions.
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                     drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                         the target prokaryotic essential genes. Note: The sequent did not form part of the printed specification, in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Xu HH;
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1 MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMVI

Query Match Best Local S Matches 445

al Similarity 445; Conserv

Conservative

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Score 2265; DI Pred. No. 2.5e 19; Mismatches

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Wall
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-PEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                          WPI; 2003-029926/02.
N-PSDB; ACA36223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klebsiella pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIT-)
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Trawick JD,
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                          Ohlsen
Forsyth
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                                                                                                                                                                                                                                                                                                                                          Zyskind JW;
Xu HH;
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression

ABO62691 ID ABO XX

AB062691

standard;

protein;

RESULT 10

Claim 25; SEQ ID NO

60277; 1766pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC polypeptide or its fragment whose expression is inhibited by the artisense nucleic acid; (4) an antibody capable of specifically binding CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of CC the gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies CC or a gene on which the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent CC product is overexpressed or underexpressed; (12) determining the extent CC strains; or (13) identifying the target of a compound that inhibits the constitution of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required constitution of an organism. The antisense nucleic acids required constitution of an organism or screening for homologous nucleic acids required constitutions.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium K. pneumoniae or P. aeruginosa. The present sequence is encoded by one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  477 AA;
                                                                                      ANARKLGDRLIVAVNSDASTKRLKGETRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
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                       IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQD 474
                                                                                                                                                                          STVSPVBLENAVRGRAETGFGVMSEBELKQAVAAARKRGEKVVMTNGVFDILHAGHVSYL
                                                                                                                                                                                                                                                                      QPGRPPLHMPTQAQEVYDVTGAGDTVIGVLAATLASGNTLEEACYFANAAAGVVVGKLGT
                                                                                                                                                                                                                                                                                                                                                       TDFERYRGATLLTPNLSEFEAVVGKCQDEAQIVERGMKLIAEFELSALLVTRSEQGMTLL
IAGILPDLLVKGGDYKPEQIAGSEEVWANGGEVLVLNFEDGCSTTNIIKKIQKD 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.1%; Score 2227; DH 6;
92.2%; Pred. No. 6.8e-192;
92.2%; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 477;
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ABO62691;

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Matches
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Best Local :
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Klebsiella pneumoniae protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-2000; 2000US-00489039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI
                    ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
                                                                                                             STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
                                                                                                                                                                                                          QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT
                                                                                                                                                                                                                                                                                                                                                                                      FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG
                                                                                                                                                                              QPGRPPLHMPTQAQEVYDVTGAGDTVIGVLAATLASGNTLEEACYFANAAAGVVVGKLGT
                                                                                                                                                                                                                                                                    TDFERYRGATLLTPNLSEFEAVVGKCQDEAQIVERGMKLIAEFELSALLVTRSEQGMTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD
                                                                                        STVSPVELENAVRGRAETGFGVMSEEELKQAVAAARKRGEKVVMTNGVFDILHAGHVSYL
                                                                                                                                                                                                                                                                                                TDFERYRGATLLTPNLSEFEAVVGKCKTBEEIVERGMKLIADYELSALLVTRSEQGMSLL
                                                                                                                                                                                                                                                                                                                                                          FEEGFSGVDPQPMHERIQQALGSIGALVLSDYAKGALTSVQTMIRLAREAGVPVLIDPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                MKVTLPEFERAGVLVVGDVMLDRYWYGPTSRISPEAPVPVVKVENIEERPGGAANVAMNI
<u>ANARKLGDRLIVAVNSDASTKRLKGETRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2227; DB 7;
Pred. No. 7.3e-192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription regulatory element; antibacterial; Vaccine.
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Ct the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid cell canding a polypeptide whose expression is inhibited by the antisense comprising a promoter operably linked to the nucleic acid cell canding the vector; (3) an isolated cell containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the polypeptide; (6) inhibited by the cell cand; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) cellular proliferation or the biological pathway in which a proliferation, or that inhibits cellular proliferation of an corganism acts; (9) manufacturing an antibiotic; (10) profiling a compound is activity; (11) a culture comprising strains in which the gene compound is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the contection of contiferation of the strains is present in a culture or collection of contiferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational content of the proliferation of notes are useful activity of acquired for proliferation in cells other than S. aureus, S. typhimurlum, the target prokaryotic essential genes. Note: The sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            문
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-PEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BLIT-)
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 73168; 1766pp; English.
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Forsyth :
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                                                       21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-PEB-2002; 2002US-0362699P.
                                                                                                                             21-MAR-2002; 2002WO-US009107
                                                                                                                                                    03-OCT-2002.
                                                                                                                                                                                                                        Antisense;
                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #35768
                                                                                                                                                                                                                                                                       19-JUN-2003
                                                                                                                                                                                                                                                                                              ABU50241;
                                                                                                                                                                                                                                                                                                                     ABU50241 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                          WO200277183-A2
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                                   (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
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                                  ELITRA PHARM
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 Zamudio
Trawick
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                                                                                                                                                                                                                                                                                                                                                                               LLVKGGDYKPEEIAGSEEVWPTGGEVMVLNFEDGCSTTNIIKKIQ 463
                                                                                                                                                                                                                                                                                                                                                                                                   LLVKGGDYKPEBIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQ 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HMPTQAQEVYDVTGAGDTVIGVLAATLAAGNTLEEACYFANAAAGVVVGKLGTSTVSPIE
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Malone C,
Carr GJ,
                                   INC.
                                                                                                                                                                                                                        essential gene; cell proliferation; drug design
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Pred. No. 4.1e-189;
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Haselbeck R, Yamamoto R,
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Ohlsen
Forsyth
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Xu HH;
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WPI; 2003-029926/02 N-PSDB; ACA54111.

New antisense nucleic acids, useful for identifying proteins or i for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs rational drug discovery programs. screening ç

Claim 25; SEQ ID NO 78165; 1766pp; English.

CC (1) a vector comprising a promoter operably linked to the nucleic acid.
CC encoding a polypeptide whose expression is inhibited by the antisense cc nucleic acid; (2) a host cell containing the vector; (3) an isolated cc polypeptide or its fragment whose expression is inhibited by the antisense cc proliferaction or the activity of a gene in an operan required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway compound that influences the activity of cidentifying a gene required for proliferation, or that inhibits cellular proliferation; (8) cidentifying a gene required for cellular proliferation or the biological pathway in which he test compound that inhibits gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the gene consideration of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational construction of solate candidate molecules for rational construction of solate candidate molecules for rational construction of the printed specification, but was obtained of all electronic format directly from WIPO at the specification, but was obtained of an electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences e invention relates to an isolated nucleic acid comprising any one of e 6213 antisense sequences given in the specification where expression the nucleic acid inhibits proliferation of a cell. Also included are:

Sequence 476 AA;

Query Match

Local

Similarity

86.8%;

Score 2076; DB 6; Pred. No. 2.9e-178;

Length 476;

밁 S 밁 S 문 S 밁 S 밁 S ঠ 문 Matches 409; 181 361 301 301 241 241 181 121 121 13 61 μ QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT SDPBRYRGATLLTPNLSEPEAVVGRCKNBBBLVNRGMQLVADFELSALLVTRSEQGMTLL ASIGANARIVGITGIDDAARAISKSIADVNVKCDFVSVPTHPTITKIRVISRNQQIIRID MKVTLPEFERAGYMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL QLGKPPLHLPTQAKEVFDVTGAGDTVIGVLAAALAAGNSLEESCFLANAAAGVVVGKLGT PEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG ASLGAVARLVGLTGIDDAARALICKLSEVRVRCDFVSVPTHPTITKLRVLSRNQQLIRLD MKVTLPDFRRAGVLVVGDVMLDRYWYGPTCRISPEAPVPVVKVDTIEERPGGAANVAMNI STVSPIBLENAIRGRAETGFGVMDEQQLKIAVAQARQRGEKVVMTNGIFDILHAGHVSYL PEEGFDGVDPTPIFERIQLALPQIGALVLSDYAKGALNSVQPMIQLARKANVPVLIDPKG Conservative 32; Mismatches Indels 0; Gaps 360 120 360 300 300 240 240 180 180 120 60 60

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RESULT 13
ABU40796
         The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid cencoding a polypeptide whose expression is inhibited by the antisense complete acid; (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated collect acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the containing the vector; (7) an isolated collect acid; (4) an antibody capable of specifically binding collideration or the activity of a gene in an operon required for compound that influences the activity of the gene product or that has an activity against a biological pathway of compound that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which has the test compound that inhibits gene product lies or a gene on which the test compound that inhibits proliferation of an compound so activity; (11) a culture or its gene product lies compound so activity; (11) a culture or collection of an compound so activity; (11) a culture or collection of compound so activity; (11) a culture or collection of strains; or (13) identifying the target of a compound that inhibits the gene compound that inhibits in which the gene conditeration of the strains is present in a culture or collection of contentifying proteins or screening for homologous nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational contents to conditate molecules for rational contents uncleic acids are useful for contents.
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06-SEP-2001;
25-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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2002US-00072851.
2002US-0362699P.
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homologous
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Best Local :
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ADF06349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
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                               standard;
                                                                                                                           IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQ 473
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                                                                                                                                                                       ANARKLGDRLI VAVNSDAS TKRLKGESR PVNPLEQRMTVLGALGAVDWVVAFBEDT PQRL
                                                                                                                                                                                                                                    STVSPIELENAIRGRADNGFGIMEESQLKQAVALARQRGERIVMTNGCFDILHAGHVSYL
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                             protein;
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82.2%; Pred. No. 5e-172;
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RESULT 14
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ID ADF066
XX ADF06
XX ADF06
XX Prote
X Proteus mirabilis Proteus mirabilis infection; bacterial infection; antibacterial; Bacterial polypeptide #2462 12-FEB-2004 09-APR-1999; 05-APR-2000; 12-AUG-2003 US6605709-B1. immunostimulant (GENO-) GENOME 2000US-00543681 (first THERAPEUTICS CORP 99US-0128706P entry)

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ABM67735
ID ABM67735
XX ABM67735
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Matches 389
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 Antibacterial, fungicide, insecticide, polymorphism,
                                                                                                           ABM67735
                                                                                                                                           ABM67735 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 491
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                                   Photorhabdus luminescens protein sequence #832.
                                                                         20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
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                                                                                                                                                                                                                                                                                                            ANARKLGDRLIVAVNSDASTKRLKGESRPVNPLEQRMTVI
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Pred. No. 5.2e-172;
43; Mismatches 41;
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genetic analysis;
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CC sources of probes and primers for detecting the genome of P. luminescens CC and related species; to study polymorphisms; for gene analysis and for Cd detection/amplification of the genes. Antibodies (Ab) raised against the CC polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that CC carry a gene-containing vector are used to select compounds that CC modulate, regulate, induce or inhibit expression of the genes in plants, CC animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. CC luminescens. Cells transformed to express the genes are useful for CC recombinant production of the proteins, particularly toxins and CC antibacterials useful as insecticides, bactericides and fungicides. The CC genes, proteins, vectors containing the genes and Ab are also useful CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence CC factors and for identifying targets of human diseases for which P. CC luminescens is a model (particularly plague and whooping cough). This
Sequence 475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to the isolation of general invention of the inventi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic sequence of Photorhabdus luminescens and encoded puseful e.g. as therapeutic antimicrobials and agricultural
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Buchrieser C;
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Matches
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MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI
                                                                  TDFBRYRGATLLTPNLSEFBAVVGKCKTBBBIVERGMKLIADYBLSALLVTRSEQCMSLL
                                                                                                                                                                                                          ASIGANARIVGITGIDDAARAISKSLADVNVKCDFVSVPTHPTITKIRVLSRNQQLIRLD
                                                  NDFERYRGATLLTPNLSEFEAVVGHCKDDNELVEKGTRLVKGLDLQALLITRSEQGMSLL
                                                                                                               FEEGFDNVDAQPMFERIEQALPHIGALVLSDYAKGALSQVQEMIKLANAAKVPVLIDPKG
                                                                                                                                            FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG
                                                                                                                                                                             AALGANSHLIGLTGIDDAAHALSEKLRSVKVRCDFVSVPTHPTVTKLRVLSRNQQLIRLD
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38; Mismatches 5
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Query Match

6

Length 475;

S 문 8

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Search completed: March 18, 2006, 06:02:33 Job time : 193 весв	421 IADVLPDVLVKGGDYKPEEIAGSEEVWAAGGDVKVLNFEDGISTTNIIKAIKNQZ 475	421 IAGILPDLLVKGGDYKPEBIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDK 475	361 ENARRIGDRLIVAVNSDASTKRIKGESRPVNPLEQRMIVLSALGAVDWVVPFEEDTPQRL 420	361 ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420	301 STVSPIELENAIRGRAETGFGVWTEFQLKQAVVDAKQRGERVVWTNGCFDILHAGHVSYL 360	301 STVSPIELENAVRGRADTGFGVMTEBELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 360	241 SVDQPPLHLPTQAQEVFDVTGAGDTVIGVLATAIAAGKPLNEACFLANAAAGVVVGKLGT 300

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Maximum DB seq length: 200000000
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Score
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                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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C81009
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probable ADP-hepto
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169	170	170.5	170.5	173.5	173.5	174	174	175	176	178	179	179.5	181.5	181.5
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309	300	343	305	300	300	316	303	311	294	306	137	383	378	148
N	- 12	N	N	N	N	N	N	N	N	ຎ	N	N	N	N
F91215	A75599	D75260	T44955	E86076	F91229	A96952	F84401	E75385	H84115	B64073	A69427	D75288	F86307	H71120
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ALIGNMENTS

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															A; Kresiques: 1-4// CDMA15 A;Cross-references: UNIPROT:P76658; UNIPARC:UPI000003EB75; GB:AE000387; A;Experimental source: strain K-12, substrain MG1655 C;Superfamily: hypothetical protein b3052	A;Status: preliminary; nucleic A;Molecule type: DNA			R;Blattner, 1	C;Species: Escherichia coli C;Date: 10-Sep-1999 #sequen	ADP-heptose N;Alternate	1
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GDRLI	GDRLI	BLENA	ELENA	LAWEL	TAMET	RGATL	RGATL	GVDPQ	GVDPQ	ARLVG	ARLVG	BFERA	BFERA	100 llarity 100 Conservative	UNIPR e: st hetic	y; nu	ine complete genome ice number: A64720; l on: B65093	.J.; Mau, B.; Sh 1453-1462, 1997	F.R.; Plunkett	#sequ	synthase homolog names: hypothetic	
VAVNS	VAVNSI	VRGRA	VRGRA	DAGEV	PAOEV	LTPNL	LTPNL	PLHER	PLHER	LIGID	LIGID	GVMVV	GVMVV	100.0%; 100.0%; tive	nces: UNIPROT:P76658; source: strain K-12, hypothetical protein	cleic	o; MU:		t III,	ence_	log - etica:	
DASTKE	DASTKG	DIGFG	OTGFGN	FDTVG	ZDTVG2	SEFEA	SEFEA	INQALS	INQALS	DAARAI	DAARAI	3DVMILE	SDVMLI	0	5658; K-12, otein	acid	WUID:9742	·		revisi	Esche l prot	
LKGDS	LKGDS	MTBEB	MTBBB	GDTVI	GDTVI	VGKCK	VGKCK	SIGAL	SIGAL	SKSLA	SKSLA	RYWYG)RYWYG	Score Pred. Mism	UNIPARC:UI substrain b3052	acid sequence	26617	h	G., Bloch,	on 10	synthase homolog - Escherichia co names: hypothetical protein b3052	
RPVNP	RPVNPI	LKCLAV	LKCLAV	GVLAA;	GVLAA:	TEERI	TEEEI	ALSDA!	VLSDY	DVNVK	DVNVX	PTSRI	PTSRI	core 2393; ced. No. 5. Mismatches	RC:UP:	nce n	A64720; MUID:97426617; PMID:9278503			#sequence_revision 10-Sep-1999	Escherichia coli protein b3052	
LEQRMI	LEQRMI	AAARKG	PAARKT	FLAAGE	[LAAG]	VERGMI	VERGMI	AKGAL	AKGAL	CDFVS	CDFVS	SPEAP	SPEAP\	DB 4e-1	PI00000 MG1655	not shown;	0:9278		C.A.; Perna,	1999 #		
VLGAL	[VI_GAL	GEKVV	GEKVV	ISLEEA	ISLEEA	CIADY	QIADY	MOOVS	MOOVS	PHHP1	I I I I I	PVVXV	VXVV4)3EB75		3503			text	(strain K-12)	
BAVDW	EAVDW	MINGV	MINGV	CFFAN	CFFAN	BLSAL	BLSAL	IQLAR	IQLAR	TKLR	ITKLR	NTIEB	NTIEB	Length 477; Indels .0	; GB:	translation not	7		N.T.; Burland,	chang	-12)	
VVSFE	WSFE!	FDILH	PDILH	AAAGV	AAAGV	LVTRS	LVTRS	KAGVP	KAGVP	VLSRN	VLSRN	RPGGA	RPGGA	477;	AB000:	ation	•		Burla	e 09-		
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															GB:U00096; NID:g]				i., co]			
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....-..eptose synthase [imported] - Escherichia coli C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 C;Accession: G91120 R;Hayashi, T.; Makino, V . Ct.
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G91120
ADP-heptose
           A;Cross-references: UNIPROT:Q8XBM4; UNIPARC:UPI00000D0591; GB:BA000007; PIDN:BAB37358.1 A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics: A;Gene: EC63935 C;Superfamily: hypothetical protein b3052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: G91120
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A;Molecule type: DNA
A;Residues: 1-477 <HAY>
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 Genome
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                                                                                                                                                                    IAGILPDLLVKGGDYKPEBIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDKKG
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Yasunaga, T.; Kuhara,
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ilarity 99.6%;
Conservative
ŏ,
enterohemorrhagic
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Pred. No. 1.7e-142;
1; Mismatches 1;
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Shiba, T.;
Escherichia
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; Hattori, M.;
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M.; Shinagawa,
0157:H7
                          J.D.; Rose,
Potamousis,
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: P85965
A;Ktatus: preliminary
A;Molecule type: DNA
A;Residues: 1-477 <STO>
A;Cross-references: UNIPROT:08XBM4; UNIPARC:UPI0000D0591; GB:AE005174; NID:g12517628;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Genetics:
A;Geneti
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                                                                                                                                                           ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
                                                                                                                                                                                                                                                                                             STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
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IAGILPDLLVKGGDYKPEBIAGSKEVWANGGEVLVLNFEDGCSTINIIKKIQQDKKG
                                                                                                                                                                                                                                                        STVSPIELENAVRGRADTGFGVMTEEELKLAVVAARKRGEKVVMTNGVFDILHAGHVSYL
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                                                                                                                          ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
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Pred. No. 1.7e-142;
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AG0891

ADP-heptose synthase (EC 2.7.-.-) [imported] - Salmonella enterica subsp. en C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AG0891 enterica

Berova

C;Accession: AG0891

C;Accession: AG0891 N.R.; Pickard, ies, R.M.; Dowd, D.; Wain, J , L.; White, J.; Churcher, e, N.; Farrar,

Skelton, J.; Salmonella e

enterica s

serova

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A; Status: preliminary

A;Molecule type: DNA
A;Residues: 1-477 <PAR>
A;Residues: 1-677 <PAR>
A;Cross-references: UNIPARC:UPI000005A4A3; GB:AL513382; PIDN:CAD07725.1; PID:g16504277; C;Genetics:
A;Gene: rfaB
C;Superfamily: hypothetical protein b3052
C;Keywords: phosphotransferase

Query Match

Score 2265; 밂 <u>ب</u> Length

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RESULT 5
A10080
A10080
AD-heptose synthase (EC 2.7.-.-) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: A10080
C;Accession: A10080
                                                                                                                                                                                                                                                                                                         A;Gene: rfaE
C;Superfamily: hypothetical protein b3052
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: Genome sequence of Yersinia pestis, the causative agent of plague. A,Reference number: AB0001; MUID:21470413; PMID:11586360 A,Accession: AI0080
                                                                                                                                                                                                                                                                                                                                                                                                        A, Molecule type: DNA
A, Residues: 1-476 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davie, P.; Dougan, G.; il. M.; Rutherford, K.; Simmonde, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: UNIPROT:Q8Z160; UNIPARC:UP100000CD706; GB:AL590842; PIDN:CAC89508.1
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Best Local
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                                                                        ASIGAVARIUGITGIDDAARALICKISEVRVRCDFVSVPTHPTITKLRVLSRNQQLIRID
                                                                                               ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD
                                                                                                                                                                       MKVTLPEFERAGYMVVGDVMLDRYWYGPTSRISPEAPVPVVXVNTIEERPGGAANVAMNI 60
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                          FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 180
                                                                                                                                                     MKVTLPDFRRAGVLVVGDVMLDRYWYGFTCRISPEAFVFVVKVDTIEERFGGAANVAMNI
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PEEGPDGVDPTP1PERIQLALPQIGALVLSDYAKGALNSVQPMIQLARKANVPVL1DPKG
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                            86.8%; Score 2076; DB 2;
86.1%; Pred. No. 4.6e-123;
*** 32; Mismatches 34;
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L9; Mismatches 12;
                                                                                                                                                                                                                                                                Length 476;
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Reference Cé4127
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP-heptose synthase homolog - Haemophilus influenzae (strain Rd KW20) C;Species: Haemophilus influenzae C;Date: 10-Sep_1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: C64127
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A; Residues: 1-476 < TIGR>
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                                                                        ELENAIHAR PETGFGIMSEABLKDAVAQAKARGEKI VMTNGCFDI LHPGHI SYLENARKL
                                                                                                                                                     YHLPTVAKEVPDVTGAGDTVISVLATALADGRSFEESCYLANVAAGIVVGKLGTSTVSTV
                                                                                                                                                                                        LHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPI
                                                                                                                                                                                                                                                    RGATILTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAP
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GDRLIVAVNSDDSVKRLKGESRPINNLENRMAVLAGLASVDWLVPFTEDTPQRLIGEILP
                                                                                                               BLENAVRGRADTGFGVMTBEBLKLAVAAARKRGEKVVMTNGVFDILHAGHVSYLANARKL
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Pred. No. 3.5e.
58; Mismatches
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rfaE protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87700
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; H
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft
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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83022
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C;Superfamily:
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A;Experimental source: strain PAO1
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A; Residues: 1-474 <STO>
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274;
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LEQVRPDVLVKGGDYGVEQVVGAQIVKAYGGEVRVLGLVENSSTTAIVEKIRQ 472
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 Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
son, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNIPARC:UPI00000C5EB9; GB:AE004912; GB:AE004091;
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n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87700
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-483 <STO>
A;Cross-references: UNIPROT:Q9A2C5; UNIPARC:UPI00000C7B50; GB:AE005673; NID:g13425394;
C;Genetics:
A;Gene: CC3640
C;Superfamily: hypothetical proteir constants.
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                                                                                              VSYLANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDT
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PLELIKAFRPDVLVKGADYTVETVVGSDVVLGYGGKVVLAELKQGQSTTNLIARM
                                                                        VSLLSQAKAACDRLIVGLNTDASVSKLKGPTRPVQKEQGRATVLASLSSVDLVVLFDEDT
                                                                                                                                              GTDVVTAAELTACASSAQGEPGEIKIADREQAQRIVEGWRARGLKVGFTNGCFDLLHPGH
                                                                                                                                                                                GTSTVSPIELEN-AVRGRADTG-FGVMTEBELKLAVAAARKRGEKVVMTNGVFDILHAGH
                                                                                                                                                                                                                    LAVRNQPPIHLPATAIEVFDVSGAGDTVAATLALAVAAGASLAQAAQLANLAGGLVVAKL
                                                                                                                                                                                                                                                      LLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKL
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RESULT H81319

probable ADP-heptose synthase Cj1150c [imported] - Campylobacter jejuni (strain C;Species: Campylobacter jejuni C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: H81319 C.; Basham, .; Whitehead l, s.; Chilling; Barrell

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; B. C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whi Nature 403, 665-668, 2000

Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter A;Reference number: A81250; MUID:20150912; PMID:10688204

A;Accession: H81319

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1116

A; Status: preliminary

A;Molecule type: DNA A;Residues: 1-461 <PAR A;Cross-references: UNIPROT:Q9PNE5; UNIPARC:UPI00000C1E38; A;Experimental source: serotype O2, strain NCTC 11168 Genetics: GB:AL139077; GB:AL111168;

;Gene: waaE; Cjl150c hypothetical protein b3052

Query Match Best Local Similarity 36.1**%**; 43.1**%**; Score Pred. 863; No. 7 DB 2; .9e-47; Length 461;

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A;Molecule type: DNA
A;Residues: 1-463 <ARN>
A;Residues: 1-463 <ARN>
A;Crose-references: UNIFROT:Q9ZKZO; UNIFARC:UPI00001337AC; GB:AE001509; GB:AE001439;
A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable adp-d-glycero-d-mannoheptose synthase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
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C;Accession: C71887

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; 1708, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.; Nature 397, 176-180, 1999

Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: C71887
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;Superfamily: hypothetical protein b3052
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                                                                                                                                                                                                                        VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLVGL 72
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                                                                                                                                                    TGIDDAARALSKSLADVNVKCDFVSV-PTHPTITKLRVLSRNQQLIRLDFBEGFEGVDP- 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFEGV
                      NADLRKNLLDFIAEKIQEIDGVILSDYNKGVLDFELTQTIITLANKHKLILCDPKGKDY
                                                                                                                                                                                                 ILVIGDLIADYYLWGKSERLSPEAPVPVLEVKKESKNLGGAANVANNLTSLKAKVFLCGV 63
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                                                                                                           VGDDLEGKHFISTLKTRGIDTSGVLIDKTRCTTLKTRIIAQNQQIVRVDKBI----KDPL 119
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RESULT 12
B64627
ADP-heptose
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G84936
Kinase [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-May-2004
C;Accession: G84936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-315 <STO>
A;Crose-references: UNIPARC:UPI000005E442; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
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R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
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C;Superfamily: ribokinase
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Local Similarity 50.0%; Pred. No. 8.7e-44;
hes 156; Conservative 63; Mismatches 93
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  Helicobacter pylori (strain 26695)
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C;Species: Helicobacter pylori
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: B44627
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: B46627
A;Accession: B46627
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H81154
ADP-heptose synthase, probable NMB0825 [imported] - Neisseria meningitidis C,Species: Neisseria meningitidis C,Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Date: H81154
C;Accession: H81154
                 A; Molecule type: DNA
A; Residues: 1-323 <TET>
A; Cross-references: Third
                                                                                                                                                   R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dought ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuc
                                                                                             A;Title: Complete genome sequence of Neisseria meningitidis A;Reference number: A81000; MUID:20175755; PMID:10710307 A;Accession: H81154
                                                                           A; Status: preliminary
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 Cross-references: UNIPROT:Q9K004; UNIPARC:UPI00000C4596; Experimental source: serogroup B, strain MC58
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Pred. No. 1.8e-43;
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                     GB:AE002435; GB:AE002098;
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C;Superfamily: ribokinase
C;Keywords: phosphotransf
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                                     LENAVRGRA 316
                                                                               YQPTRAQEVYDVSGAGDTVIAGMGLGLAAGCTMPEAMYLANTAAGVVVAKLGTAVCSFAE
                                                                                                                                                              GATLITPNRAELKEVVGSWKNESELTEKAQNLRRHLDLTÄVLLTRSEEGMTLFSEGE-PI
                                                                                                                                                                                    GATILITPNISEPEAVVGKCKTEEEIVERGMKLIADYELSALIVTRSEQGMSILQPGKAPL
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321
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Pred. No. 3.7e-40;
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R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Nature 404, 502-506, 2000 probable DP-heptose synthetase (BC 2.7.-.-) NMA1034 [imported] - Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004 C;Accession: H81951 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis A;Reference number: A81775; MUID:20222556; PMID:10761919 phosphotransferase RLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFBEGFEG EVLEQIKRKYREILPEYDAIIFSDYGKGGLSHISDMIDWAKHEGKTVLIDPKGDDYEKYA VDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKGTDFERYR GATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAPL GLLSVTGNDEAADALDALMVQDGVASYLMRDKQIATTVKLRVVARNQQLIRLDFEEHPNR FAQAKVLVVGDVMLDRYWFGDVSRISPEAPVPVAKIGRIDQRAGGAANVARNIASLGGKV FERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANA Conservative 31.2%; 49; Mismatches 103; Score 745.5; DB 2 Pred. No. 1.2e-39; UNIPARC:UPI00000445DA; strain Z2491 DB 2; Indels Length GB:AL162754; 1; Gaps GB:AL157959; 247 193 133 73 67 S.R.; Morell Rajandream,

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Bubmitted to the EMBL Data Library, February 1999
A,Reference number: Z21559
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C/Species: Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Spate: 5-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Gene: SCOEDB:SC2G5.08
;Superfamily: hypothetical protein b3052
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;Experimental source: strain A3(2)
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Residues: 1-463 <OLI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 RYRGATLITPNISEFEAVVGKCKTE-----EBIVERGMKLIADYBISALIVTRSEQGM 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 ----RVREATDEARDALGCARAVLVSDYGRGAADALRDVL----AARPPLVWDPHPRGGP 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 24.8%; Score 594; DB 2; Length 463; Similarity 36.3%; Pred. No. 6.5e-30;
                                                                                                                                                                TPORLIAGILPDILLVKGGDYKPEBI -- AGSKEVWANGGEVLVLNFEDGCSTTNIIKK 470
                                                                                                                                                                                                                      HVGLLQAARRLGDCLVVCVNSDASVRRGKGGGRPVNPLADRVRVLRALACVDAVAVFDED 402
                                                                                                                                                                                                                                                                                                                                GGAAAVPPAGSERALAALPDTD------DPGALAARIRAEHGTVVAAGGCFDLLHAG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                           ALLSYGEHPLLVPAPAAHHGDSCGAGDRFAATAAGLLADGALVGEAVEGAVGAATAFVAA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLLOPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGK 297
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                                                                                                          TPERLIGELRPDVWVKGGDYAGADLPBAGLLKEW--GGQAVLLPYLDGRSSTALLAR 457
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Gapop 10.0 , Gapext 0.5
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                                                     O6luzs photobacter Q8deh7 vibrio vuln O7mny3 vibrio vuln Q87sj9 vibrio para Q7vm30 haemophilus Q5e217 vibrio fisc Q8eaz2 shewantella Q7vqq6 candidatus Q4uf0 azotobacter Q4zz1s pseudomonas Q87vf4 pseudomonas Q80d93 pseudomonas
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Q8fdh5 escherichia
Q7aaq7 escherichia
Q7ubi8 shigella fl
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Q6d164
Q665v3
Q8z160
Q7n0c3
Q8g1u7
Q65t41
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Result No.

Database

Searched:

Sequence:

Run on:

	Q607m3 Q83b60 Q74bf80 Q5p280 Q5f852 Q9a2c5 Q9m2c1 Q6m9u1 Q6m9u1
Q607M3 METCA HLDE CÖXBU HLDE GBOSL Q5P250 AZOSE Q5PS52 GLUOX HLDE CAUCR HLDE CAUCR HLDE WOLSU HLDE BRAJA ALHIT3 CAMLA Q4HIT3 CAMLA	, XW
	Q607m3 Q83b60 Q74bf6 Q5p852 Q5f852 Q9a2c5 Q7m9u1 Q6m2r5 Q6m2r5 Q6m2r3 Q8b2r3 Q8b2r3 Q8b2r3

ALIGNMENTS

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	to D-glycero-D-manno-hept	-369(2002). -369(2002). -369(2002).		"The riak gene from ESCHETICNIA COLI encodes a Diffunctional process involved in the biosynthesis of the lipopolysaccharide core precursor ADP-L-glycero-D-manno-heptose."; J. Bacteriol. 182:488-497(2000). [3] FUNCTION, AND ADP-L-BETA-D-HEPTOSE BIOSYNTHESIS PATHWAY.	INS. INS-12 / W1485; INE-20096694; PubMed-10629197; DOI-10.1128/JB.182.2.488- ano M.A., Marolda C.L., Bittner M., Glaskin-Clay M., Sim	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. STRAIN=K12 / MG1655; MEDLINE=97486617; PubMed=9278503; DOI=10.1126/science.277.5331.1453; MEDLINE=97486617; PubMed=9278503; DOI=10.1126/science.277.5331.1453; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).	2.7.1) (D-beta-D-heptose 7-phosphotransfephosphate adenosyltransferase (BC 2.7.7)). Synonyms=rfaE, waaE; OrderedLocusNames=b305 a coli. Proteobacteria; Gammaproteobacteria; Enteroberiaceae; Escherichia.	ECOLI BCOLI P76658; P76658; 15-JUL- 15-JUL- 10-MAY- Bifunct

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Query Match
Best Local 9
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InterPro; IPR004820; CytIdylylTransf.

InterPro; IPR004820; CytIdylylTransf.

InterPro; IPR001173; PfkB region.

InterPro; IPR011913; RfaE_dom_I.

InterPro; IPR011914; RfaE_dom_I.

InterPro; IPR011914; RfaE_dom_I.

InterPro; IPR011915; RfaE_dom_I.

IfterPro; IPR011915; Cyt_transf_2; 1.

Pfam; PP00294; PfkB; 1.

TIGRPAMS; TIGR00195; Cyt_tran rel; 1.

TIGRPAMS; TIGR02199; rfaE_dom_I; 1.

TIGRPAMS; TIGR02199; rfaE_dom_I; 1.

PROSITE; PS00584; PFKB_KINASES_1; 1.

PROSITE; PS00584; PFKB_KINASES_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cirbohydrate metabolism; Complete proteome; Kinase; Lipopolysaccharide biosynthesis; Multifunctional en Nuclectidyltransferase; Transferase; REGION 1 318 Ribokinase.

REGION 344 477 Cytidylyltransferase.
SEQUENCE 477 AA; 51051 MW; 0F03CBE160B95389 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EchoBASE;
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PATHWAY: Inner core lipopolysaccharide biosynthesis; ADP-L-
glycero-beta-D-manno-heptose biosynthesis; fourth step.
MISCELLANEOUS: In both reactions the enzyme functions only with
beta anomers.
MISCELLANEOUS: The function of the domain II is independent from
MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
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SIMILARITY: In the C-terminal section;
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EG13416; hldE.
                                                                 STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
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                                                                                                                                                       QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT
                                                                                                                                                                                                                                          TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL
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ANARKLGÜRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
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Cytidylyltransferase.
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                                                                                InterPro; IPR004821; Cyt trans rel.
InterPro; IPR004820; CytIdylyltransf.
InterPro; IPR002173; PfkB.
InterPro; IPR011611; PfkB region.
InterPro; IPR011913; RfaE dom I.
InterPro; IPR011914; RfaE dom II.
InterPro; IPR011914; RfaE dom II.
Pfam; PP00467; CTP transf 2; 1.
Pfam; PP00467; PfkB; 1.
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25-OCT-2004 (Rel. 45, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Bifunctional protein hldE [Includes: D-beta-D-heptose 7-phosphate
kinase (EC 2.7.1.-) (D-beta-D-heptose 7-phosphotransferase); D-beta-D-heptose 1-phosphate adenosyltransferase (EC 2.7.7.-)].
Name-hldE; Synonyms=rfaE; OrderedLocusNames=c3800;
Bscherichia coll 06.
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25-OCT-2004
25-OCT-2004
10-MAY-2005
TIGRPAMB; TIGRO0125; cyt tran_rel; 1
TIGRPAMB; TIGRO2198; rfaE_dom_I; 1.
TIGRPAMB; TIGRO2199; rfaE_dom_II; 1.
PROSITE; PS00583; PFKB_KINASES_1; 1.
                                                                                                                                                                                                                                                            HAMAP;
                                                                                                                                                                                                                                                                                                                                                                                        This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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SIMILARITY: In the C-terminal section; belongs
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P27623; 1COZ.
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Best Local (
                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN-0157:H7 / EDL93 / ATCC 700927 / EHEG.

MEDLINE-21074935, PubMed-11206551, DOI-10.1038/35054089;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.,

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                               THIDE ECO57 STANDARD; PRT; 477 AA.

(7)AAQ7; Q8XBM4;
25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
23-SEP-2005 (Rel. 45, Last sequence update)
B1functional protein hldE [Includes: D-beta-D-heptose 7-phosphate
kinase (EC 2.7.1.-) (D-beta-D-heptose 7-phosphotransferase); D-beta-D-heptose 1-phosphate adenosyltransferase (EC 2.7.7.-)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGION
REGION
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE, P800584; PFKB KINASES 2; FALSE NEG. Carbohydrate metabolism; Complete proteome; Kinas Lipopolysaccharide biosynthesis; Multifunctional Nucleotidyltransferase; Transferase.
                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                 Name-hldE; Synonyms-rfaE; OrderedLocusNames-z4405,
Escherichia coli O157:H7.
                                                                                                                                                                                                              I_TaxID=83334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANARKLGDRLI VAVNSDASTKRLKGDSRPVNPLEQRMI VLGALEAVDWVVSFEEDTPQRL
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477 AA;
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Cytidylyltransferase.
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Pred. No. 5.8e-134;
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                                                                                                                                                                                                                                                     Enterobacteriales
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Matches
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Best Local :
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TIGRPAMS; TIGR02198; rfaE_dom_I; 1.
TIGRPAMS; TIGR02198; rfaE_dom_I; 1.
TIGRPAMS; TIGR02199; rfaE_dom_I; 1.
PROSITE; P800584; PFKB_KINASES_1; 1.
PROSITE; P800584; PFKB_KINASES_2; FALSE_NEG.
Carbohydrate metabollsm; Complete proteome; Kinase;
Lipopolysaccharide biosynthesis; Multifunctional enzym
Nucleotidyltransferase; Transferase.
Nucleotidyltransferase; Transferase.
REGION 344 477 Cytidylyltransferase.
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REGION
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yobe T Han C.-G., Ohtsubo B., Nakayama K., Murata T., Tanaka M., Tobe I ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli ol57.H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01467; CTP trai
Pfam; PF00294; PfkB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_01603; -; 1
InterPro; IPR004821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; F85965; F85965
PIR; G91120; G91120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE005174; AAG58186.1; -; EMBL; BA000007; BAB37358.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] STRAIN=0157:H7 / Sakai / RIMD 0509952 / EHEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 8:11-22(2001)
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InterPro, IPR011913; RfaE dom I.
InterPro, IPR011914; RfaE dom II.
Pfam; PP01467; CTP transf_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interPro;
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CANALYTIC ACTIVITY: ATP + D-glycero-beta-D-manno-heptose 7-phosphate = ADP + D-glycero-beta-D-manno-heptose 1,7-bisphosphate.
CANALYTIC ACTIVITY: ATP + D-glycero-beta-D-manno-heptose 1-phosphate = diphosphate + ADP-D-glycero-beta-D-manno-heptose 1-phosphate = diphosphate + ADP-D-glycero-beta-D-manno-heptose.
pathway: Inner core lipopolysaccharide biosynthesis; ADP-L-phosphate - heptose-pathway: Inner core lipopolysaccharide biosynthesis - heptose-pathway: Inner core lipopolysaccharide biosynthesis - heptose-pathway: Inner core lipopolysaccharide biosynthesis - heptose-pathwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycero-beta-D-manno-heptose biosynthesis; second step.
PATHWAY: Inner corre lipopolysaccharide biosynthesis; ADP-L-
glycero-beta-D-manno-heptose biosynthesis; fourth step.
SIMILARITY: In the N-terminal section; belongs to the carbol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Catalyzes the phosphorylation heptose 7-phosphate at the C-1 position bisphosphate (By similarity).
FUNCTION: Catalyzes the ADP transfer to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as long as its content is
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SIMILARITY:
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                                                                                                                                                                                                                                                                                                      475;
       61
                                                                          61
                                                                                                                                                                                                                                                                                                                                              Similarity
                                               ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLTRLD
                                                                                                                                                                                            MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI
                                                                                                                                                         MKVTLPEFERAGVMVVGDVMLDRYWYGPSSRISPEAPVPVVKVNTIEERPGGAANVAMNI
       ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR004821; Cyt trans_rel.
IPR004820; Cytidylyltransf.
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477
                                                                                                                                                                                                                                                                                                      Conservative
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99.6%;
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                                                                                                                                                                                                                                                                                                      Score 2385; D
Pred. No. 6.6e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribokinase.
Cytidylyltransferase.
; BB877FEF6636E67C CRC64;
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Genomic_DNA
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form D,D-heptose-1,7-
                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme
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M., Tobe T.,
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EMBL

a collaboration -MBL outstation -

outstation

9 is not

carbohydrate

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HLDE SHIFL

HLDE SHIFL

HLDE SHIFL

AC O7UBIS, 083047;

AC O7UBIS, 083047;

AC O7UBIS, 083047;

DT 25-CCT-2004 (Rel. 45, Last sequence update)

DT 25-CCT-2004 (Rel. 45, Last sequence update)

DT 35-SEP-2005 (Rel. 48, Last amotation update)

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      WEDLINE=22590274; PubMed=12704.152;

WMEDLINE=22590274; PubMed=12704.152;

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WMEDLINE=22590274; PubMed=12704.152;

WA A Gournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,

WA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,

WA A Schwartz D.C., Blattner F.R.;

WINCOMPLETE SETTING AND COMPARATIVE GENOMICS OF Shigella

RT flexneri serotype 2a strain 2457T.";

Infect. Immun. 71:2775-2786 (2003).

-1- FUNCTION: Catalyzes the phosphorylation of D-glycero-D-manno-heptose 7-phosphate at the C-1 position to form D,D-heptose-1,7-

C heptose 7-phosphate at the ADP transfer to D-glycero-D-manno-heptose

1-phosphate, yielding AND-D,D-heptose (By similarity).

C -1- CATALYTIC ACTIVITY: ATP + D-glycero-beta-D-manno-heptose 1-

phosphate = ADP + D-glycero-beta-D-manno-heptose 1-

phosphate = diphosphate + ADP-D-Jlycero-beta-D-manno-heptose 1-

phosphate: The CTIVITY: ATP + D-glycero-beta-D-manno-heptose 1-

PATHWAY: Inner core lipopolysaccharide biosynthesis; ADP-L-
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InterPro; IPR004821; CytIdylylTransf.

InterPro; IPR004820; CytIdylylTransf.

InterPro; IPR004820; PfkB.

InterPro; IPR0018213; PfkB.

InterPro; IPR011913; RfaE_dom_II.

InterPro; IPR011914; RfaE_dom_II.

InterPro; IPR011914; RfaE_dom_II.

Pfam; PF01294; PfkB; 1.

Pfam; PF00294; PfkB; 1.

Pfam; PF00294; PfkB; 1.

Pfam; PF00294; PfkB; 1.

ITGRPAMs; TIGR02198; rfaE_dom_I; 1.

TIGRPAMs; TIGR02198; rfaE_dom_I; 1.

TIGRPAMs; TIGR02198; rfaE_dom_I; 1.

PROSITE; PS00584; PFKB_KINASES_1; 1.

PROSITE; PS00584; PFKB_KINASES_2; PALSE_NEG.

Carbohydrate metabolism; Complete proteome; Kinase; Lipopolysaccharide biosynthesis; Multifunctional en:
Nucleotidyltransferase; Transferase.

REGION

1 318

Cytidyltransferase
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PATHWAY: Inner core lipopolysaccharide biosynthesis; ADP-L-
glycero-beta-D-manno-heptose biosynthesis; fourth step.
SIMILARITY: In the N-terminal section; belongs to the carbol
kinase pfkB family.
SIMILARITY: In the C-terminal section; belongs to the
cytidylyltransferase family.
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.", Nature 413:848-852(2001).
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Burland V., Kodoyianni V., Schwartz D
"Comparative genomics of Salmonella e
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25-OCT-2004 (Rel. 45, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Bifunctional protein hidE [Includes: D-beta-D-heptose 7-phosphate
kinase (EC 2.7.1.-) (D-beta-D-heptose 7-phosphotransferase); D-beta-D-heptose 1-phosphate adenosyltransferase (EC 2.7.7.-)].
                                                                                                                                                                                                                                                                                                                              This Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8XEW9; Q7AM91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol. 185:2330-2337(2003).
- FUNCTION: Catalyzes the phosphorylation of heptose 7-phosphate at the C-1 position to
                                                                                                                                                                                                                                                                                                                                                                                                                                          bisphosphate (By similarity).

bisphosphate (By similarity).

rUNCTION: Catalyzes the ADP transfer to D-glycero-D-manno-heptose (By similarity).

l-phosphate, yielding ADP-D,D-heptose (By similarity).

cATALYTIC ACTIVITY: ATP + D-glycero-beta-D-manno-heptose 7-phosphate = ADP + D-glycero-beta-D-manno-heptose 1.

cATALYTIC ACTIVITY: ATP + D-glycero-beta-D-manno-heptose 1.

phosphate = diphosphate + ADP-D-glycero-beta-D-manno-heptose.

phosphate = diphosphate + ADP-D-glycero-beta-D-manno-heptose biosynthesis; ADP-L-glycero-beta-D-manno-heptose biosynthesis; ADP-L-glycero-beta-D-
                                                                                                                                                                                                                                                              8 Swiss-Prot entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                kinase pfkB family.
SIMILARITY: In the C-terminal section; belongs
                                                                                                                                                                                                                                                                                                                                                                                  cytidylyltransferase family.
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                                                                                                                                       AL627278; CAD07725.1; -;
AE016844; AA070663.1; -;
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P27623; 1....

MF 01603; -; 1.

Pro, IPR004821; Cyt trans_rel.

Pro, IPR004820; CytIdylyltransf.
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Schwartz D.C., Blattner F.R.;
almonella enterica serovar Typ
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form D,D-heptose-1,7-
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                                                                                                                                                                                                                                                                                         Q7CPR9; Q9AJ74; Q9RFY7; Q9RFY8;
25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Bifunctional protein hids [Includes: D-beta-D-heptose 7-phosphate
kinase (EC 2.7.1.-) (D-beta-D-heptose 7-phosphotransferase); D-beta-D-heptose 1-phosphate adenosyltransferase (EC 2.7.7.-)].
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TIGRPANS; TIGRO2198; rfaB_dom_I; 1.
TIGRPANS; TIGRO2199; rfaB_dom_II; 1.
PROSITE; PS00583; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; PAN_PROSITE; PS00584; PFKB_KINASES_2; PAN_PROSITE; PS00584; PFKB_KINASES_3; PAN_PROSITE; PS00584; PAN_PROSITE; PS00584; PAN_PROSITE; PS00584; PAN_PROSITE; PS00584; PAN_PROSITE; PS00584; PAN_PROSITE; PAN_PROSITE; PS00584; PAN_PROSITE; PAN_PR
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InterPro; IPR011913; RfaE_dom I.
InterPro; IPR011914; RfaE_dom_II
Pfam; PF01467; CTP transf_2; I.
Pfam; PF00294; PfkB; 1.
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InterPro;
InterPro;
                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Bnterobacteriaceae; Salmonella.
                                                                                                                                                                                                                          Name=hldE; Synonyme=rfaE,
Salmonella typhimurium.
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Lipopolysaccharide biosynthesis; Multifunctional enzyme;
Nucleotidyltransferase; Transferase.
NUCLEOTIDE SEQUENCE, AND ROLE IN LPS BIOSYNTHESIS PubMed=12441667; DOI=10.1023/A:1021103501626;
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Q9RFY7; Q9RFY8;
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Pred. No. 9
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R InterPro; IPR004821; CytIdylylTransf.

R InterPro; IPR004821; CytIdylylTransf.

R InterPro; IPR002173; PftB.

R InterPro; IPR011914; RfaE_dom_I.

R InterPro; IPR011914; RfaE_dom_I.

R InterPro; IPR011914; RfaE_dom_I.

R InterPro; IPR011914; RfaE_dom_I.

R Ffam; PF00467; CTP_transf_2; 1.

R Pfam; PF00294; PftB; 1.

R TIGRPAMs; TIGR00125; cyt_tran_rel; 1.

R TIGRPAMs; TIGR02199; rfaE_dom_I; 1.

R TIGRPAMs; TIGR02199; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN-LT2 / SGSC1412 / ATCC 700720;

MEDILINE-21534948; PubMed=1167769; DOI=10.1038/35101614;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., I
COurtney L., Porwollik S., Ali J., Dante M., Du F., Hou &
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., M
Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan

Waterston R., Wilson R.K.;
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MEDLINE=20096694; PubMed=10629197; DOI=10.1128/JB.182.2.488-497.2000
Valvano M.A., Marolda C.L., Bittner M., Glaskin-Clay M., Simon T.L.,
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between the Swi
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                                                                                                                                                                                                                                                                                                                                                                                         1COZ.
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Best Local :
STRAIN-SC-B67;
PubMed=15781495;
Chiu C.-H. Tang P., Ci
Wang H.-S., Lee Y.-S.;
"The genome sequence
highly invasive and re
Nucleic Acids Res. 33:
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Q57JQ9;
10-MAY-2005
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VARIANT
                                                                                                                                                                                Name=rfaE; OrderedLocusNames=SC3147;
Salmonella cholerae-suis (Salmonella enterica).
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Salmonella.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Putative sugar nucleotide transferase domain of ADP-L-glycero-D-manno-
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A McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,

A Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McL

A Harkins C.R., Wang C., Mgyen C., Berghoff A., Elliott G.,

A Kohlberg S., Strong C., Du P., Carter J., Kremizki C., Ley

A Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,

A Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,

A Delbhaunty K., Fronick C., Magrini V., Nhan M., Warren W.,

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Comparison of genome degradation in Paratyphi A and Typhi

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Nat. Genet. 36:1268-1274(2004).

R EMBL, CP000026; AAV79903.1.; -; Genomic DNA.

R GO; GO:0016779; F:kinase activity; IEA.

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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
ADP-haptose synthase.
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GO; GO:0009103; P:lipopolysaccharide biosynthesis;
InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR004821; Cyt_trans_rel.
InterPro; IPR004821; Cyt_trans_rel.
InterPro; IPR011611; PfkB region.
InterPro; IPR011913; RfaE_dom_I.
InterPro; IPR011914; RfaE_dom_II.
InterPro; IPR011914; RfaE_dom_II.
Pfam; PF01467; CyTp_transf_2; I.
Pfam; PF01467; CyTp_transf_2; I.
ITGRPAMs; TIGR012198; rfaE_dom_I; 1.
ITGRPAMs; TIGR02199; rfaE_dom_I; 1.
ITGRPAMs; TIGR02199; rfaE_dom_II; 1.
PROSITE; PS00583; PFKB_KINASES_1; 1.
                                                                                        QGD14;
25-CCT-2004 (TrEMBLrel. 28, Created)
25-CCT-2004 (TrEMBLrel. 28, Last sequence update)
25-CCT-2004 (TrEMBLrel. 28, Last annotation update)
25-CCT-2004 (TrEMBLrel. 28, Last annotation update)
ADP-heptose synthase (EC 2.7.-.-)
Name-rfa8; Synonyms-was8; OrderedLocusNames=ECA3584;
Erwinia carotovora (subsp. atroseptica) (Pectobacterium :
Batteria; Proteobacteria; Gammaproteobacteria; Enterobact
Enterobacteriaceae; Pectobacterium.
                                                                                                                                                                                                                         LT 9
64 ERWCT
Q6D164 ERWCT
    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN-SCRI 1043 / ATCC BAA-672;
PubMed=15263089; DOI=10.1073/pnas.0402424101;
Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G
Holeva M.C., Thomson N.R., Bentley S.D., Churcher
                                                                                  NCBI_TaxID=29471;
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EMBL; BX950851; CAG76482.1; -; Genomic_DNA.

R GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0016779; F:nucleotidyltransferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0009058; P:biosynthesis; IEA.

GO; GO:0009059; P:carbohydrate metabolism; IEA.

GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.

InterPro; IPRO1151; Cyt transf.

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CONTAINATION SEQUENCE [LARGE SCALE GENOMIC DNA].

CONTAINATION SERVICE SERVICE STATEMENT F.W., Lamerdin J., Stoutl Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutl Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Moctin Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Moctin Regala W.M., Georgescu A.M., Vergez L.M., Madigu Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Ell Proc. Math. Acad. For Proc. I.M., Dacheux D., Ell Derbise A., Hauser L.J., Garcia E.;

"Insights into the evolution of Yersinia pestis through who comparison with Yersinia pseudotuberculosis.;

Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).

EMBL; BEN936398; CAM22645.1; -; Genomic DNA.

GO; GO:0016779; F.nucleotidyltransferase activity; IEA.

GO; GO:0016779; F.nucleotidyltransferase activity; IEA.

GO; GO:0016779; F.nucleotidyltransferase activity; IEA.

GO; GO:0016779; F.nucleotidyltransf.

GO; GO:0016799; F.transferase activity; IEA.

GO; GO:0016799; F.transferase activity; IEA.

GO; GO:0016799; F.transferase activity; IEA.

RO; GO:0016799; F.transferase activity; IEA.

RO; GO:0016799; F.transferase.

RINTERPORT IFR0011913; RÉB_dom_II.

RINTERPORT IFR0011913; RÉB_dom_II.

RETIGRAMS; TIGR02199; RÉB_dom_II.

Pfam; PP01467; CTP transf_2; 1.

RETIGRAMS; TIGR02199; RÉB_dom_II.

RETIGRAMS; TIGR02199; RÉB_dom_II.

RETIGRAMS; TIGR02199; RÉB_dom_II.

RETIGRAMS; TIGR02199; RÉB_MINASE_I; 1.

ROGOSOS3; PRES KINASE_I; 1.

Complete proceome; Transferase.

SEQUENCE 476 AA; 51202 MW; E56550CA2D31726D CRC64;
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Best Local :
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Yersinia pseudotuberculosis
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Last annotation ADP-heptose synthase (EC 2.7.-.-).
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                                        IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDK
                                                                                                                                                                                    ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
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Pred. No. 8
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, Medigue C.,
D., Elliott
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between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no

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RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Zhou D., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
Yang H., Wang J., Huang P., Yang R.,
RA Yang H., Wang J., Huang P., Yang R.,
RA Yang H., Wang J., Huang P., Yang R.,
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(98ZIĞ), (94ZAS);

25-OCT-2004 (Rel. 45, Created)

25-OCT-2004 (Rel. 45, Last sequence update)

10-MAY-2005 (Rel. 47, Last annotation update)

Bifunctional protein hidz [Includes D-beta-Pheptose 7-phosphate kinase (EC 2.7.1.-) (D-beta-D-heptose 7-phosphotransferase); D-beta-D-heptose 1-phosphate adenosyltransferase (EC 2.7.7.-)].

Name=hidz; Synonyms=rfaz, wasz;

OrderedLocusNames=YPO0654, y3524, YP2969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perry R.D.;

Mayhew Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,

Straley S.C., McDonough K.A., Nilles M.L., Matson J.S.,

Perry R.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA)
STRAIN*KIM5 / BIOVAR MEDILEVAL18;
MEDILNE=22137863; PubMed=12142430;
DOI=10.1128/JB.184.16_4601-4611.2002;
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STRAIN=CO-92 / Blovar Orientalis;
MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
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Bacteria, Proteobacteria, Gammaproteobacteria,
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J. Bacteriol. 184:4601-4611(2002).
                                                                     kinase pfkB family.
SIMILARITY: In the C-terminal
                                               cytidylyltransferase
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                                                  family.
                                                                        section;
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R Pfam; PP01294; PfkB; 1.

R TIGRPAMS; TIGR00125; Cyt tran rel; 1.

R TIGRPAMS; TIGR02195; rfaE_dom_I; 1.

R TIGRPAMS; TIGR02195; rfaE_dom_I; 1.

R TIGRPAMS; TIGR02195; rfaE_dom_I; 1.

R PROSITE; PS00583; PPKB KINASES_1; 1.

R PROSITE; PS00584; PPKB KINASES_2; FALSE NEG.

R PROSITE; PS00584; PPKB KINASES_1; 1.

R PROSITE; PS00584; PPKB KINASES_1; ALSE NEG.

R PROSITE; PS00584; PPKB KINASES_1; 1.

R PROSITE; PS00584; PPKB KINASES_1; 1.

R PROSITE; PS00584; PPKB KINASES_1; 1.

R PROSITE; PS00584; PPKB KINASES_1; ALSE NEG.

KW Lipopolysaccharide biosynthesis; Multifunctional enzym Nucleotidyltransferase; Transferase.

FT REGION 344 476

Cytidylyltransferase.

FT REGION 344 476

Cytidylyltransferase.

FT REGION 344 476

CYTIGROUPH AND TRANSFERAME.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR011611; PfkB region.
InterPro; IPR011913; RfaE_dom_I.
InterPro; IPR011914; RfaE_dom_II.
Pfam; PP01467; CTP_transf_2; I.
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                                                   IAGILPDLLVKGGDYKPEBIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDK
                                                                                                             ANARKLGDRLIVAVNSDASTKRLKGEKRPVNPLEQRMVVLGALEAVDWVVPFEEDTPQRL
                                                                                                                                                                                                                     STVSPIBLENAIRGRAETGFGVMDEQQLKIAVAQARQRGEKVVMTNGIFDILHAGHVSYL
                                                                                                                                                                                                                                                                                                                                QLGKPPLHLPTQAKEVPDVTGAGDTV1GVLAAALAAGNSLEESCFLANAAAGVVVVGKLGT
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AAM87072.1; ALT_INIT; Genomic_DNA
AAS63148.1; ALT_INIT; Genomic_DNA
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Cytidylyltransferase.
; E68FF382DC892636 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2076; DB 1;
Pred. No. 1.7e-115;
2; Mismatches 34;
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Best Loc
Matches
                                                                                                                                                     PhotoList; plu3968; -.

HAMAP; MF 01603; -; 1.

InterPro; IPR004821; Cyt trans_rel.

InterPro; IPR004821; Cyt dylyltransf.

InterPro; IPR001611; PfkB region.

InterPro; IPR011513; RfaE_dom I.

InterPro; IPR011914; RfaE_dom_II.

InterPro; IPR011914; RfaE_dom_II.

InterPro; IPR011914; RfaE_dom_II.

Pfam; PP01467; CTP transf_2; 1.

Pfam; PP0294; PfkB; 1.

Pfam; PP0294; PfkB; 1.

ITGRPAMs; TIGR00125; cyt tran_rel; 1.

TIGRPAMs; TIGR02199; rfaE_dom_I; 1.

TIGRPAMs; TIGR02199; rfaE_dom_I; 1.

PROSITE; PS00583; PFKB_KINASES_1; 1.

PROSITE; PS00583; PFKB_KINASES_1; 1.

PROSITE; PS00584; PFKB_KINASES_2; PALSE_NEG.

                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Blotechnol. 21:1307-1313(2003).

-i- FUNCTION: Catalyzes the phosphorylation of D-glycero-D-manno-heptose 7-phosphate at the C-1 position to form D,D-heptose-1,7-bisphosphate (By similarity).

-i- FUNCTION: Catalyzes the ADP transfer to D-glycero-D-manno-heptose 1-phosphate, yielding ADP-D,D-heptose (By similarity).

-i- CATALYTIC ACTIVITY: ATP + D-glycero-beta-D-manno-heptose 1-phosphate = ADP + D-glycero-beta-D-manno-heptose 1-phosphate = ADP + D-glycero-beta-D-manno-heptose 1-phosphate = ADP + D-glycero-beta-D-manno-heptose 1-phosphate = ADP+D-glycero-beta-D-manno-heptose 1-phosphate = ADP-D-glycero-beta-D-manno-heptose.
-i- PATHWAY: Inner core lipopolysaccharide biosynthesis; ADP-L-glycero-beta-D-manno-heptose.
-i- PATHWAY: Inner core lipopolysaccharide biosynthesis; ADP-L-glycero-beta-D-manno-heptose biosynthesis; Fourth step.
-i- SIMILARITY: In the N-terminal section; belongs to the carbohydrate kinase pikB family.
-i- SIMILARITY: In the C-terminal section; belongs to the cytidylyltransferase family.
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10-MAY-2005 (Rel. 47, Last amnotation update)
Bifunctional protein hidE [Includes: D-beta-D-heptose 7-phosphate
kinase (EC 2.7.1.-) (D-beta-D-heptose 7-phosphotransferase); D-beta-D-
heptose 1-phosphate adenosyltransferase (EC 2.7.7.-)].
Name-hidE; Synonyms-rfaE; OrderedLocusNames-plu3968;
Photorhabdus luminescens (subsp. laumondi).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A., Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F., Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S., Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.; "The genome sequence of the entomopathogenic bacterium Photorhabdu luminescens.";
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                                                                                         SEQUENCE
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51130
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  37;
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Score 1949; DB 1;
Pred. No. 6.2e-108;
7; Mismatches 52;
                                                                                       Ribokinase.
Cytidylyltransferase.
, DC4C4E30D10E862D CF
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                                                RX MEDLINE-S 4074 / Serctype 1;

RX MEDLINE-S 4074 / Serctype 1;

RA Provost M., Harel J., Labrie J., Sirois M., Jacques M.;

RA Provost M., Harel J., Labrie J., Sirois M., Jacques M.;

RY Tidentification, cloning and characterization of rfag of ridentification, 

RY Inpoplotyses the phosphorylation of D-glycero-D-manno-heptose -1,7-cc heptose 7-phosphate (probable).

CC -I-FUNCTION: Catalyzes the ADP transfer to D-glycero-D-manno-heptose 7-cc -1-phosphate (probable). Phosphose (Probable).

CC -I-CATALYTIC ACTIVITY: ATP + D-glycero-beta-D-manno-heptose 1,7-bisphosphate.

CC -I-CATALYTIC ACTIVITY: ATP + D-glycero-beta-D-manno-heptose 1-phosphate = diphosphate + ADP-D-glycero-beta-D-manno-heptose.

CC -I-PATHWAY: Inner core lipopolysaccharide biosynthesis; ADP-L-cc glycero-beta-D-manno-heptose biosynthesis; ADP-L-cc -I-PATHWAY: Inner core lipopolysaccharide biosynthesis; ADP-L-cc -I-CXIMILARITY: In the N-terminal section; belongs to the carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8GLÜ7;
25-OCT-2004
25-OCT-2004
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25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Bifunctional protein hldE [Includes: D-beta-D-heptose 7-phosphate kinase (EC 2.7.1.-) (D-beta-D-heptose 7-phosphotransferase); D-bet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
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SIMILARITY:
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RR InterPro; TRROU4821; CYLTIdylylTransf.

RR InterPro; TRROU2173; PfKB.

RR InterPro; TRROU2173; PfKB region.

RR InterPro; TRROU1913; RfaB_dom_I.

RR InterPro; TRROU1913; RfaB_dom_I.

RR InterPro; TRROU1914; RfaB_dom_I.

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RPfam; PP01467; CTP transf_2; T.

Pfam; PP01467; CTP transf_2; T.

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InterPro; IPR004821; Cyt trans_rel.
InterPro; IPR011611; PfkB region.
InterPro; IPR011913; RfaB_dom_I.
InterPro; IPR011914; RfaB_dom_II.
Pfam; PF01467; CTP_transf_2; I.
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TIGRPAMS; TIGR02199; rfaE_dom_II; 1.
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Name=rfaE; OrderedLocusNames=MS1262;
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EMBL; AE016827; AAU37869:1; -; Genomic_DI
GO; GO:0016779; F:nucleotidyltransferase
GO; GO:0009058; P:biosynthesis; IEA.
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Bacteria; Proteobacteria; Gammaproteobacteria;
Pasteurellaceae; Mannhelmia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKGTDFERY 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQLLGLTGLDETGKALTTLLQTQKIDCDFVRLATHPTITKLRILSRHQQLLRLDFEEDFK
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                        DLLVKGGDYKPEBIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDK
                                                                                                    QFNQAKVLVLGDVMLDRYWFGATNRISPEAPVPVVRVQENEERAGGAANVAMNIASLNVP
                                                                                                                                                      GDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRLIAGILP
                                                                                                                                                                                                         ELENAIHGRSSTGFGIMNEDELKVAVQLAKARGEKIVMTNGCFDILHPGHVSYLENARKL
                                                                                                                                                                                                                                                                                                                                                                                                                         RGATLLTPNMSEFEAVVGKCDTEEDIIEKGLKLIADIELSALLVTRSEKGMTLLRPGQEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1727; DB 2;
Pred. No. 1.1e-94;
4; Mismatches 75
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-I-FUNCTION: Catalyzes the phosphorylation of D-glycero-D-manno-heptose 7-phosphate at the C-1 position to form D,D-heptose-1,7-bisphosphate (Probable).

-I-FUNCTION: Catalyzes the ADP transfer to D-glycero-D-manno-heptose 1-phosphate, yielding ADP-D,D-heptose (Probable).
-I-CATALYTIC ACTIVITY: ATP + D-glycero-beta-D-manno-heptose 7-phosphate = ADP + D-glycero-beta-D-manno-heptose 1-phosphate = ADP + D-glycero-beta-D-manno-heptose 1-phosphate = diphosphate + ADP-D-glycero-beta-D-manno-heptose 1-phosphate = diphosphate + ADP-D-glycero-beta-D-manno-heptose 1-glycero-beta-D-manno-heptose biosynthesis; ADP-L-glycero-beta-D-manno-heptose biosynthesis; ADP-L-glycero-beta-
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Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D., McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D., McKenney K., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D., Weidman J.F., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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10-MAY-2005 (Rel. 47, Last annotation update)
Bifunctional protein hids [Includes: D-beta-D-heptose 7-phosphate
kinase (EC 2.7.1.-) (D-beta-D-heptose 7-phosphotransferase); D-beta-D-
heptose 1-phosphate adenosyltransferase (EC 2.7.7.-)].
Name=hidE; Synonyms=rfaE, waaE; OrderedLocusNames=HI1526;
                                                                                                                                               InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                EMBL; U32828; AAC23172.1;
EMBL; U17642; AAC43516.1;
PIR; C64127; C64127.
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[2]
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STRAIN=NTH1 2019;
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influenzae 2019 rfaE gene
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Lee N.-G., Sunshine M.G., Apicell
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"Whole-genome random sequencing
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STRAIN=Rd / KW20 / I
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.-G., Sunshine M.G., Apicella M.A., lecular cloning and characterization (luenzae 2019 rfaE gene required for 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytidylyltransferase family.
CAUTION: Ref.2 sequence differs from that shown frameshift in position 331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European
p; HI1526; -. 1.

P; MF_01603; -; 1.

rPro; IPR004821; Cyt trans_rel.

rPro; IPR004820; CytIdylyltransf.

rPro; IPR002173; PfkB.

rPro; IPR011611; PfkB_region.

rPro; IPR011914; RfaE_dom_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Swiss-Prot
                                                                                                                                                                                                                                                P27623; 1COZ.
HI1526; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rot entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation - Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63:818-824(1995).
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DR Pfam; PF00146/;
DR Pfam; PF00294; PfkB; 1.

DR TICRPAMS; TIGR00125; Cyt tran rel; 1.

TICRPAMS; TIGR00125; Cyt tran rel; 1.

DR TICRPAMS; TIGR001299; rfaE dom I; 1.

DR TICRPAMS; TIGR02199; rfaE dom I; 1.

DR PROSITE; PS00583; PFKB KINASES 1; PALSE NEG.

PROSITE; PS00584; PFKB KINASES 2; PALSE NEG.

DR PROSITE; PS00584; PFKB KINASES 2; PALSE NEG.

KW Carbohydrate metabolism; Complete proteome; Kinase;

KW Multifunctional enzyme; Nucleotidyltransferase.

FT REGION 344 476 Cytidylyltransferase.

FT REGION 36 36 A -> R (in Ref. 2).

FT CONFLICT 84 84 L -> H (in Ref. 2).

FT CONFLICT 170 170 A -> G (in Ref. 2).

FT CONFLICT 273 273 A -> T (in Ref. 2).

FT CONFLICT 273 273 A -> C (in Ref. 2).

TOMPLICT 278 278 R -> C (in Ref. 2).

TOMPLICT 278 278 R -> C (in Ref. 2).
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31; Conservative
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                    DLLVKGGDYKPEBIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQ
                                                                                        GDRLIVAVNSDASTKRIKGDSRPVNPIBQRMIVLGALBAVDWVVSFBEDTPQRLIAGILP
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DLLVKGGDYKPEBIAGSKEVWANGGDVKVLNFENGCSTTNVIEKIK
                                                               GDRLIVAVNSDDSVKRLKGESRPINNLENRMAVLAGLASVDWLVPFTEDTPQRLIGETLP
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71.0%;
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Pred. No. 8.2e
58; Mismatches
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Search completed: March 18, 06:06:28

time

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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         US-09-492-709A-325
US-09-489-039A-9208
US-09-543-681A-6634
US-09-477-962-114
US-09-489-039A-9668
US-09-252-991A-31882
US-09-134-000C-4524
US-09-134-001C-4521
US-09-668-262A-14
US-09-688-262A-16
US-09-688-262A-16
US-09-688-262A-16
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Sequence 9208, App
Sequence 6634, App
Sequence 32984, A
Sequence 114, App
Sequence 9668, Ap
Sequence 31882, A
Sequence 4524, Ap
Sequence 1275, Ap
Sequence 1275, Ap
Sequence 1275, Appl
Sequence 11, Appl
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12, Appl
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	Sequence 11526, A	Sequence 16334, A	Sequence 8628, Ap	Sequence 5214, Ap	Sequence 8124, Ap	Sequence 22565, A	Sequence 7290, Ap	Sequence 7111, Ap	Sequence 10377, A	Sequence 21413, A	Sequence 281, App	Sequence 4544, Ap	Sequence 17, Appl	Sequence 4, Appli	Sequence 10, Appl	Sequence 2, Appli	Sequence 5583, Ap	Sequence 10221, A	
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ALIGNMENTS

RESULT 1 US-09-492-709A-325

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241 QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT 	181 TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL 	121 FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 	61 ASIGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD	1 MKVTLPEFERAGYMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI 	Query Match 100.0%; Score 2393; DB 2; Length 477; Best Local Similarity 100.0%; Pred. No. 5.8e-232; Matches 477; Conservative 0; Mismatches 0; Indels 0	Sequence 325, Application US/09492709A Patent No. 6720139 GENERAL INFORMATION: APPLICANT: Zyskind, Judith APPLICANT: Zyskind, Judith APPLICANT: Ohleen, Kari L. APPLICANT: Forsyth, R. Allyn APPLICANT: Forsyth, R. Allyn APPLICANT: Forsyth, R. Allyn APPLICANT: Yamamoto, Robert T. APPLICANT: Yamamoto, Robert T. APPLICANT: Yam, H. Howard TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION TITLE OF INVENTION: SCHESICHIA COLI TITLE REFERENCE: ELITEA.001A CURRENT APPLICATION NUMBER: US/09/492,709A CURRENT APPLICATION NUMBER: US/09/492,709A CURRENT OF SEQ ID NOS: 485 SOFTWARE: FRATSOFT 495 SEQ ID NO 325 LENGTH: 477 TYPE: PRT ORGANISM: E. Coli US-09-492-709A-325
		GVPVLIDPKG OPVLIDPKG	SRNOQLIRLD		7; 0; Gaps	ATION IN
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 2709.2004001
CURRENT PILLING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: US 60/117,747
PRIOR RILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9208
LENGTH: 499
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
S-09-489-039A-9208
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Best Local Similarity
Matches 437; Conserv
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GENERAL INFORMATION:
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Pred. No. 3.3e-215;
Pred. No. 3.3e-215;
Mismatches 12;
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Application US/09543681A

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GENERAL INFORMATION:

APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO E

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO E

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32984

LENGTH: 526

TYPE: PRT
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US-09-252-991A-32984
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILITILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6634
                                                                                                                                                                                                                                                                                                Sequence 32984, Application US/09252991A Patent No. 6551795
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Pred. No. 4.6e-193;
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                                                                                                ; TYPE: PRT
ORGANISM: Streptomyces verticillus
FEATURE:
OTHER INFORMATION: ORF9
US-09-477-962-114
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US-09-252-991A-32984
                                                                                                                                                                           NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn Ver. 3
SEQ ID NO 114
LENGTH: 498
                                   Matches
                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SHEN, BEN
APPLICANT: DU, LIANGO
APPLICANT: SANCHEZ, C
APPLICANT: CHEN, MEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 114, Application US/09477962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 57.9 Matches 274; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 692728
                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/118,848 PRIOR FILING DATE: 1999-02-05
                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 407T-895820US
CURRENT APPLICATION NUMBER: US/09/477,962
CURRENT FILING DATE: 2000-01-05
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/115,435 PRIOR FILING DATE: 1999-01-06
                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: EDWARDS, DANIEL J.

TILE OF INVENTION: BLEOMYCIN GENE CLUSTER COMPONENTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TDFERYRGATLLTPNLSEFEAVVGKCKTEBEIVERGMKLIADYBLSALLVTRSEQGMSLL
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                                 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 MKLSMPRFDQAPVLVVGDVMLDRYWHGATSRISPEAPVPVVRVEQHEDRPGGAANVALNI
 13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLVGL 72
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SANCHEZ, CESAR
CHEN, MEI
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                                 Conservative
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37.7%;
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                               ; Score 610.5; DB 2; pred. No. 2.1e-52; 68; Mismatches 196;
                                 Indels
                                                               Length 498;
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                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SEQ ID NO 9668
LENGTH: 342
TYPE: PRT
                                                                                                                                                                                                                                                 Query Match
Best Local
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APPLICANT: Gary Br
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 GVPVLIDP---KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEBIVERGMKLIADYELSA 227
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; ORGANISM: Klebsiella pneumoniae US-09-489-039A-9668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEFULICANT: GATY Breton et. al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERADDITATION OF THE DEPENDENCE.
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133 DAENMIAVD-----PGANMIVTDDEIAGCIPAIGCADVVLVQLENNLSAIEQVIDAGKQA
                                                                       114 -- QQLIRLDFEEGFEGVDPQPLHERINQALSSIG-ALVLSDYAKGALASVQQMIQLARKA 170
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                                                                                                                                                                                                                   55 NVAMNIASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTH-PTITKLRVLSRN 113
                                                                                                                                                                                                                                                                                       17 RAALP---RAGIEERMMSGKVCVFGSFNFDMVARVD-RFPVPGESLVACGSMTSAGGKGA 72
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                                                                                                                                                   73 NQATAALKAGANVHYIGKIGNDTFGHFARRHLKGVGFNAVTLLVAEETPTGNALIYVAGN 132
                                                                                                                                                                                                                                                                                                                                                           2 KVTLPEFERAGV---MVVGDV-MLDRYWYGPTSRISPEAPVP---VVKVNTIEERPGGAA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 26.9
90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   8.2%; Score 197; DB 2; 3.26.9%; Pred. No. 5.1e-11; ative 52; Mismatches 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 342;
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RESULT 8
US-09-134-000C-4524
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US-09-252-991A-31882
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US-09-252-991A-31882
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              GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPI
FILE REFERENCE: 032796-032
                                                                                                    Sequence 4524, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
NUMBER OF SEQ ID NOS: 331
SEQ ID NO 31882
LENGTH: 503
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Patent No. 6551795
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Best Local
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FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
CURRENT FILING NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 PSLERGWNKDATMQAKVLVVGSLNMDLVVRAPRLPRGGE----TLAGQSFTTIPGGKGAN
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                                                                                                                                                                                                                                                                                                                  SALLVTRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACF 285
                                                                                                                                                                                                                                                                                                                                                  TVILNPAPATRDVPADWLPLVDYLVPNETESELL---CRLPVDSLESAGRAAERLREMGA
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                                                                                                                                                                                                                                                                                                                                                                                                                        QNAIVIVAGGNGHLSPAVLARHEHLLEQ-----AQVVVVCQLESPLETVGHVLRRAHALGK
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                                                                                                                                                                                                             FGQAAAAISVTRLGAQTSIPSREEVERALAGEA
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1998-07-27
NUMBER: US/09/134,000C
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RESULT 9
US-09-543-681A-7498
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                                                                                                                                                                                                                                                                                                                                     US-09-543-681A-7498
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: GARY BRETON
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING '
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7498
LENGTH: 311
TYPE: PRT
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PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7498, Application Patent No. 6605709
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TYPE: PRT
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                                                                                                                                                                                                                                     y Match 7.6%;
Local Similarity 24.3%;
nes 63; Conservative 4
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Local Similarity 24.5%;
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                                              FVNQQGENVIGIHAGANGRLNREYVERYNSVIKKADALLMQ--LESPLDSVLKAAQVAKQ
                                                                                             SRNQQLIR-LDFEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARK 169
                                                                                                                                            GKGANQAVAAGRCGANITFLACLGNDDIGQSAKAQLITDKIDTDCIEL-IDDEATGVALI 102
                                                                                                                                                                                         GGAANVAMNIASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVL 110
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AGVPVLIDP----KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELS
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; Pred. No. 1.1e-09;
47; Mismatches 141
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Pred. No. 4.8e-10;
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RESULT 11
US-09-668-262A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SEQ ID NO 12757
LENGTH: 356
                                                                                                                                                                                                                            Sequence 14, Application US/09668262A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                   Patent No. 6596926
GENERAL INFORMATION:
APPLICANT: Palco, Carl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
PPLICANT: Rafalski, Antoni
ITLE OF INVENTION: Phosphatidylcholine Biosynthetic Enzyme
ILE REFERENCE: BB1403 US NA
URRENT APPLICATION NUMBER: US/09/668,262A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         307 ELENAVRGRADTGFGVMTEBELKLAVAAAR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 LHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 LTPNLSEF-----BAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAP 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ARLGIDCSLIQRTALKETSATILPIRPNGERPALHCRGASDALPVSEAEFDAVLDCRFLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 PTSRISPEAPVPVVKVNTIEERPGG-AANVAMNIASLGANARLVGLTGIDDAARALSKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLPSVDYFMPSLEEAAFLSGETQPEAIGRFFLALG---VGTCILKDGENGSWLIGRDGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H-----GGTGLLAAMDQGQSA-----RLLQAAKARGVTTSFDLIAPNEETLELLRP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPV---LIDPKGTDFERYRGATL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADVNVKCDEV8------VPTHETITKLRVLSRNQQLIRLDEBEGEEGV-DEQELH
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                                                                                                     Famodu, Omolayo O.
Kinney, Tony
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                                                                                                                                                                                                                                                                                                                                                        GVVDWEQTQAFMAAHR 355
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US-09-668-262A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Oryza sativa US-10-427-442-14
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PRIOR FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 20
SOPTWARE: Microsoft Office 95
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                              Query Match 7.1%; Score 169; DB 2; Length 423; Best Local Similarity 30.5%; Pred. No. 4.8e-08; Matches 67; Conservative 24; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Office 95
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 696070
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/155626
PRIOR FILING DATE: 1999-09-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/427,442
CURRENT FILING DATE: 2003-05-01
PRIOR APPLICATION NUMBER: US/09/668,262A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Falco, Carl
APPLICANT: Famodu, Omolayo O.
APPLICANT: Kinney, Tony
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Phosphatidylcholine Biosynthetic Enzyme
FILE REFERENCE: BB1403 US NA
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                                                                                389 PVNPLEQRMIVLGALEAVDWVVSFEEDTP----
                                                                                                                                                                                  329 KLAVAAARKRGEKVVMTNGVFDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDSR 388
                                                                                                                                                                                                                                                                                274 LAAGNSLEEACFFANAAAGVVVGKLGTSTVS----PIELENAVRGRADTGFGVMTEEEL 328
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                                                                                                                                    ----RRGRRRPVRVYM-DGCFDMMHYGHCNALRQARALGDELIVGVVSDHEITANKGP---
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                                 VRAVKWVHDVIPDAPYAITEDFMNKLFNEYNIDYIIHGDDPCLLPD 160
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RESULT 14
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                              Sequence 4521, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
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LENGTH: 665
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APPLICANT: Lynn Doucette-Stamm et TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Klebsiella
09-489-039A-8800
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
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Local Similarity 22.5%;
les 120; Conservative 9
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                                                                                                                                                                                                                                                                                                                                 HLHRVTSRRQQWPELCIFAFD-----HRKQLADLARETGRDEACIPQLKLLLLAAAEAAA 431
                                                                                                                                                                                                                                                                                                                                                                       LAVAAARKRGEKVVMTNGVFDILHAGHVSYLAN-ARKLGD-----RLIVAVNSDAST 380
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  AMINO ACID SEQUENCES RELATING TO
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US-09-489-039A-14043
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CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14043
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14043, Application Patent No. 6610836
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS FILE REFERENCE: GTC-007
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                                       GKGANQAVAAGRSGADIAFIACTGDDDIGERIRRQLASDKI-----DVAPVRAV
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Result
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AB01698 Shigella
Continuation (32 o
AR385308 Sequence
AL627278 Salmonell
AB016844 Salmonell
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ALIGNMENTS

RESULT 1
BD268493
LOCUS
DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM ORIGIN FEATURES COMMENT REFERENCE TITLE AUTHORS JOURNAL Bource C12N1/15, PC C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/02,C12Q1/68 PC ,G01N33/15,G01N33/50, PC G01N33/53,G01N33/566,C12N15/00,C12N5/00 PC G01N33/53,G01N33/566,C12N15/00,C12N5/00 BD268493 1434 bp DNA linear PAT 17-JUL-2003 Gene identified as being necessary in growth of Escherichia coli. C12N15/09, A61K31/7088, A61K48/00, A61P31/04, C07K14/245, C07K16/12, BD268493 BD268493.1 GI:33078 JP 2002535007-A/165. PN JP 2002535007-A/165
PD 22-OCT-2002
PP 27-JAN-2000 JP 2000596147
PR 27-JAN-1999 US 60/117405
PI JUDITH ZYSKIND, KARI L OHLSIN, JOHN TRAWICK, ALLYN
JAMIE M FROELICH, GRANT J CARR, ROBERT T YAMAMOTO, HOWARD H XU source /organism='E. coli'. Location/Qualifiers /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644" COLI Location/Qualifiers
1. .1434 growth of Escherichia Ħ FORSYTH PI

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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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            GCTTCTCTCGGTGCTAATGCACGCCTGGTCGGGTTGACGGGCATTGACGATGCAGCGCGC
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GTTAAAGTGAATACCATCGAAGAACGTCCGGGCGGCGCGCGAACGTGGCGATGAATATC
                                                                                                    CTGGATCGTTACTGGTACGGCCCCACCAGTCGTATCTCGCCGGAAGCGCCGGTGCCCGTG
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/mol_type="unassigned DNA"
/db_xref="taxon:562"
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 1260 1260	1201 GGCGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAGAGGGACACGCCCGCAGCGCTTG
1200	1141 AAACGGCTGAAAGGGGATTCCCGCCCGGTAAACCCCACTCGAACAGCGTATGATTGTTGCTG
1140 1140	. 1081 GCAAATGCCCGCAAGCTGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCCTCCACC
1080	1021 AAAGTGGTGATGACCAACGGTGTCTTTGACATCCTGCACGCCGGGCACGTCTCTTATCTG
 1020	961 GGCGTGATGACCGAAGAGGAACTGAAGCTGGCCGTAGCGGCAGCGCGTAAACGTGGTGAA
960	901 TCCACGGTTTCGCCGATCGAGCTGGAAAATGCTGTACGTGGACGTGCAGATACAGGCTTT
900	841 GAAGAAGCCTGCTTTGCCAATGCGGCGGCTGGCGTGGTGGTCGGCAAACTGGGAACC
840 840	781 GGTGCGGGCACACGGTGATTGGCGTCCTGGCGGCAACGCTGGCAGCGGGTAATTCGCTG
780 780	721 CAACCGGGTAAAGCGCCGCTGCATATGCCAACCGAAGCGCAGGAAGTGTATGACGTTACC
720 720	661 GCCGATTACGAACTCTCCGGCTCTGTTAGTGACCCGTTCCGAACAGGGTATGTCGCTGCTG
660	601 GCTGTTGTCGGTAAATGTAAGACCGAAGAAGAGATTGTTGAGCGCGGCATGAAACTGATT
 600	541 ACCGATTTTGAGCGCTACCGCGGCGCTACGCTGTTAACGCCGAATCTCTCGGAATTTGAA
 540	481 CAGCAGATGATCCAACTGGCGCGTAAAGCGGGTGTTCCGGTGCTGATTGAT
480 480	421 CTGAGTTCGATTGGCGCGCTGGTGCTTTCTGACTACGCCAAAGGTGCGCTGGCAAGCGTA
420 420	361 TTTGAAGAAGGTTTCGAAGGTGTTGATCCGCAGCCGCTGCACGAGCGGATTAATCAGGCG
 360 360	301 CATCCGACCATTACCAAATTACGGGTACTTTCCCGCAACCAAC
 300	241 GCGCTGAGTAAATCTCTGGCCGACGTCAACGTCAAATGCGACTTCGTTTCTGTACCGACG

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Zyskind, J., Ohlsen, K.L., Trawick, J., Forsyth, R.A., Froelich, J.M., Carr, G.J., Yamamoto, R.T. and Xu, H.H.

Genes identified as required for proliferation in Escherichia coli Patent: US 6720139-A 165 13-APR-2004;

Elitra Pharmaceuticals, Inc.; San Diego, CA
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ACCGATTTTGAGCGCTACCGCGGCGCTACGCTGTTAACGCCGAATCTCTCGGAATTTGAA
                                                        GCGCTGAGTAAATCTCTGGCCGACGTCAACGTCAAATGCGACTTCGTTTCTGTACCGACG 300
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                                   Escherichia coli
Escherichia coli
Bacteria, Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                                                                     Sequence 276 from AX189075
 Forsyth, R.A., Ohlsen, K.L. Genes identified as requi:
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Blitra Pharmaceuticals, Inc.
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    GCCGATTACGAACTCTCGGCTCTGTTAGTGACCCGTTCCGAACAGGGTATGTCGCTGCTG
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/translation="MKVTLPEFERAGVMVVGDVMLDRYMYGPTSRISPEAPVPVVKVN
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GNSLEEACFPANAAAGVVVGKLGTSTVSFIELEKNAVGAGDTVGGVMTEEELKLAVAA
ARKRGEKVVMTNGVFDILHAGHVSYLANARKLGBRLIVAVNSDASTKRLKGDSRFVNP
LEQRMIVLGALEAVDMVVSFEEDTFQRLIAGILPDLLVKGGDYKFBEIAGSKEVWANG
GEVLVLNFEDGCSTTNIIKKIQQDKKG"
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	JOURNAL FEATURES	REPERENCE AUTHORS TITLE	SOURCE ORGANISM	LOCUS DEFINITION ACCESSION VERSION KEYWORDS	RESULT 5	B Q	B 8	B &				\$ B	\$ B	Q	g - 29	B &	B 8	. g	& <u>8</u>	?
/or /mo /db	Patent: EP 1178052-A 165 06-PEB-2002; Elltra Pharmaceuticala, Inc. (US) Location/Qualifiers 1. 1434		Escherichia coli Bacherichia coli Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceas, Escharichia.	AX363670 1434 bp DNA linear PAT 15-FEB-2002 V Sequence 165 from Patent EP1178052. AX363670 AX363670.1 GI:18695784		1381 GGTTGCTCGACCACCACATCATCAAGAAGATCCAACAGGATAAAAAAGGCTAA 1434 	1321 GCCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGAC 1380	1261 ATCGCCGGGATCTTGCCAGATCTGCTGGTGAAAGGCGGCGACTATAAACCAGAAGAGATT 1320 1261 ATCGCCGGGATCTTGCCAGATCTGCTGGTGAAAGGCGGCGACTATAAACCAGAAGAGATT 1320	OI GGCGCACTGGAAGCGGTCGACTGGGTAAGTGTCGTTTGAAGAGGACACGCCGCAGCGCTTG 12	ADACGGCTGAAAGGGGATTCCCGCCCGGTAAACCCCACTCGAACAGCGTATGATTGTGCTG		1021 AAAGTGGTGATGACCAAGGTGGCTTTGACATCCTGCACGCGGGCACGTCTCTTATCTG 1080 1021 AAAGTGCCCGCAAGCTGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCCTCCACC 1140	961 GGCGTGATGACCGAAGAGGAACTGAAGCTGGACGCCGTAGCGGCAGCGCGTAAACGTGGTGAA 1020 1021 AAAGTGGTGATGACCAACGGTGTCTTTGACATCCTGCACGCCGGGCACGTCTCTTATCTG 1080	61 GGCGTGATGACCGAAGAGGAACTGAAGCTGGCCGTAGCGGCAGCGCGGTAAACGTGGTGAA	901 TCCACGGTTTCGCCGATCGAGCTGGAAAATGCTGTACGTGGACGTGCAGATACAGGCTTT 960 	841 GAAGAAGCCTGCTTCTTTGCCAATGCGGCGGCTGGCTGGTCGTCGGCAAACTGGGAACC 900	781 GTGCGGGCGACACGGTGATTGGCGTCCTGGCGGCACCGCTGCAGCGGGTAATTCGCTG 840		bl GCUGATTAGGAGCICTGGGTTAGTGACCCGTTCCGAAGAGAGTATGTCGCTGCTG 720 721 CAACCGGGTAAAGCGCGCTGCATATGCCAAGCCAAGCGCAGGAAGTGTTTGACCTTACC 780	
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                                                                                                                                                                                                                                                                                                                                                           Submitted (01-JUN-1995) Guy Plunkett, Laboratory of Genetics, University of Wisconsin, 445 Henry Mail, Madison, WI 53706, USA On Feb 27, 1996 this sequence version replaced 91:882576.

This sequence was determined as part of the E. coli Genome Project (Prederick R. Blattner, director) at the University of Wisconsin-Madison. Supported by award H600301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli MG1655, overlaps with other sequence determinations are annotated. The end of this entry overlaps the start of the entry ECOUW67 (U18997) by 1596 bp. This entry should be considered somewhat provisional; it will be updated and merged with others at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli
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1 (bases 1 to 25638)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plunkett,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECU28379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTGCTCGACGACCAACATCAACAAGATCCAACAGGATAAAAAAAGGCTAA 1434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCGCCGGGATCTTGCCAGATCTGCTGGTGAAAGGCCGCGACTATAAACCAGAAGAGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACGGCTGAAAGGGGATTCCCCGCCCGGTAAACCCCACTCGAACAGCGTATGATTGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAACGGCTGAAAGGGGATTCCCCGCCCGGTAAACCCACTCGAACAGCGTATGATTGTGCTG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAAATGCCCGCAAGCTGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCCTCCACC 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCGCCGGGATCTTGCCAGATCTGCTGGTGAAAGGCGGCGACTATAAAACCAGAAGAGATT 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAGAGGACACGCCGCAGCGCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTTGCTCGACGACCAACATCATCAAGAAGATCCAACAGGATAAAAAAGGCTAA 1434
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                                                           /codon_start=1
/transI_table=
                                                                                                 note="alternate name
                                                                                                                                                                                                                          gub.
                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                     xref="taxon:562"
                                                                                                                                                                                                                                                                _type="genomic
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                                                                                                                                       subcloning"
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sfgfgrshiapaitelyrnypelqvhfelfdrqidlvqbnidlibildigibelfpyyah
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Vsghlssnsgeivlowalegkgimlrsewpvlpflesgklvqvlpeyaqsaniwavyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:882580"
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GCFQCLALWPGFSRSGATISGGMLMGVSRYAASEFSFLLAVPMMMGATALDLYKSWGF
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TRRRIAAVASWKEQRCPKPE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLDDKQRTIIMQWFMYGGGVLGLGLLLGLVLPHLIESRKRKDRWMN"
<6237. .8494
                                                                                                                                                                                                                                                                                          complement(10119. .11051)
/note="alternate name ygi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARAANVGVIIERGNNLKENN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (8455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTSGDIPMFAVGFITAFVVALIAIKTFLQLIKRISFIPFAIYRFIVAAAVYVVFF"
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/gene="bacA"
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KTLTDKLTNI DNTWNQRTAEMQQKVAQSDS VI NGLKEENQKLKNELI VAQKKVDAAS V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (9016. .9387)
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                                                                                                                                                          /protein_id="AAA89140.1"
/db_xref="GI:1203799"
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/db_xref="GI:882581"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1/transI_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=
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transI_table=11
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                                                                                                                                                                                                                               transl_table=11/
                                                                                                                                                                                                                                                             codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                id="AAA89139.1"
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                                                                                                                                                                                                                                                                                       ygiP; ORF_310"
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                                                                                                                        14862. .19917
/notem"similar
(ECORPSRPO)"
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/note="similar to (
(ECOTATTDAB)"
                                                                                                                                                                                                                                                                                                                                                                                                                                         IGLMKSASHATLSWGDWFLGMLPLSILLVLLVPWLAYVLYPPVLKSGDQVPRWAETEL
QAWGPLCSREKRWLGLWVGALVLWIFGGDYIDAAMVGYSVVALMLLLRIISWDDIVSN
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FFASATAYTSALAPMIAAALAMPEIPLPVFCLWVGAALGLGSILTFYATGPSPIYYG
SGYLPTADYYRLGAIFGLIFLYLLVITGLLWMPVVLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EATVKAPLRHNAVEIFDEVNTGKNTGSGVPWVTWDIIPDNDDAEIEVYMAGGGCTLPG
RSKVLMPSEGYEGVVKFVFENISTLAVNACPPVLVGVGIATSVETAAVLSRKAILRPI
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Aageapdktakllgldypggpllskmaaqgtagrpvpprpmtdrpgldpspsglktfpa
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(ECORPSU) "
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               GCCGATTACGAACTCTCGGCTCTGTTAGTGACCCGTTCCGAACAGGGTATGTCGCTGCTG
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Db 3536 CTGGATCGTTACTGGTACGGCCCCTCCAGTCGTATCTCGCCGGAAGCGCCGGTGCCCGTG 3477 Qy 121 GTTAAAGTGAATACCATCGAAGAACGTCCGGGCGGCGGCTAACGTGGCGATGAATATC 180	RESULT 9 ABO05174 40/c WPCOMMENT Sequence split into 56 fragments LOCUS ABO05174 Accession ABO05174
3596 ATGAAAGTAACGCTGCCAGAGTTTGAACGTGCAGAAGTGATAGTGGTGGTGGTGATGTGATG	QY 1381 GGTTGCTCGACGACCAACATCATCAAGAAGATCCAACAGGATAAAAAAGGCTAA 1434
Query match 90.0%; Scote 1307.0; De 1; Dength 110000; Best Local Similarity 98.0%; Pred. No. 0; Matches 1405; Conservative 0; Mismatches 29; Indels 0; Gaps 0; NATCHARAGETANCGCTGCCAGAGTTTGAACGTGAATGGTGGTTGGTTGATGTGATG	Qy 1321 GCCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGAC 1380
05174-55 5500001 5528445 105174 T41 of 56) of AE005174 from base 4000001 (AE005174	QY 1261 ATCGCCGGGATCTTGCCAGATCTGCTGGAAAGGCGGCGACTATAAACCAGAAGAGATT 1320
005174_51 5100001 005174_52 5200001 005174_53 5300001	Qy 1201 GGCGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAGAGGACACGCCGCAGCGCTTG 1260
005174_47 4700001 005174_48 4800001 005174_49 4900001 005174_50 5000001	Qy 1141 AAACGGCTGAAAGGGGATTCCCGCCCGGTAAACCCACTCGAACAGCGTATGATTGTGCTG 1200
005174_43 4300001 005174_44 4400001 005174_45 4500001 005174_46 4600001	Qy 1081 GCAAATGCCCGCAAGCTGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCCTCCACC 1140
005174 ³ 9 3900001 005174 ⁴ 0 4000001 005174 ⁴ 1 4100001 005174 ⁴ 2 4200001	Qy 1021 AAAGTGGTGATGACCAACGGTGTCTTTGACATCCTGCACGCCGGGCACGTCTCTTATCTG 1080
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005174_27 2700001 005174_28 2800001 005174_29 2900001 005174_30 3000001	OY 841 GAAGAAGCCTGCTTCTTTGCCAATGCGGCGCTGGCTGGTCGGCAAACTGGGAACC 900
005174_23 2300001 005174_24 2400001 005174_25 2500001 005174_26 2600001	QY 781 GGTGCGGGCGACACGGTGATTGGCGTCCTGGCGGCAACGCTGGCAGCGGGTAATTCGCTG 840
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005174_03 300001 41000 005174_04 400001 51000 005174_05 500001 61000	Qy 481 CAGCAGATGATCCAACTGGCGCGTAAAGCGGGTGTTCCGGTGCTGATTGAT
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ATAAAAAAGGCTAA 1434 ||||||||||| NTAAAAAAGGCTAA 2163

TGGTGCTCAACTTTGAAGAC 1380 ||||||||| |TGGTGCTCAACTTTGAAGAC 2217

ACTATAAACCAGAAGAGATT 1320 CTACAAACCGGAAGAGATC 2277

1201 GGCGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAGAGGACACGCCGCAGCGCTTG 1260	1141 AAACGGCTGAAAGGGGATTCCCGCCCGGTAAACCCACTCGAACAGCGTATGATTGTGCTG 1200	1081 GCAAATGCCCGCAAGCTGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCCTCCACC 1140	1021 AAAGTGGTGATGACCAACGGTGTCTTTGACATCCTGCACGCCGGGCACGTCTCTTATCTG 1080	961 GGCGTGATGACCGAAGAGGAACTGAAGCTGGCCGTAGCGGCAGCGCGTAAACGTGGTGAA 1020 	901 TCCACGGTTTCGCCGATCGAGCTGGAAAATGCTGTACGTGGACGTGCAGATACAGGCTTT 960 	841 GAAGAAGCCTGCTTCTTTGCCAATGCGGCGGCTGGCTGGTGGTCGGCAAACTGGGAACC 900	781 GGTGCGGGCGACACGGTGATTGGCGTCCTGGCGGCAACGCTGGCAGCGGGTAATTCGCTG 840	721 CAACCGGGTAAAGCGCCGCTGCATATGCCAACCCAAGCGCAGGAAGTGTATGACGTTACC 780	661 GCCGATTACGAACTCTCGGCTCTGTTAGTGACCCGTTCCGAACAGGGTATGTCGCTGCTG 720	601 GCTGTTGTCGGTAAATGTAAGACCGAAGAGAGATTGTTGAGCGCGGCATGAAACTGATT 660 	541 ACCGATTITGAGCGCTACCGCGGCGCTACCGCTGTTAACGCCGAATCTCTCGGAATTTGAA 600	481 CAGCAGATGATCCAACTGGCGCGTAAAGCGGGTGTTCCGGTGCTGATTGAT	421 CTGAGTTCGATTGGCGCGCTCGGTGCTTTCTGACTACGCCAAAGGGTGCGCTGGCAAGCGTA 480	361 TITGAAGAAGGTTTCGAAGGTGTTGATCCGCAGCCGCTGCACGAGCGGATTAATCAGGCG 420 	301 CATCCGACCATTACCAAATTACGGGTACTTTCCCGCAACCAAC	241 GCGCTGAGTAAATCTCTGGCCGACGTCAACGTCAAATGCGACTTCGTTTCTGTACCGACG 300	GCTTCTCTCGGTGCTAATGCACGCCTGGTCGGGTTGACGGCATTGACGATGCAGCGCGC	3416. THE THE RESTRICT OF STREET OF
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	cps	gene	FEATURES source	TITLE	REFERENCE	TITLE JOURNAL	AUTHORS	ORGANISM REFERENCE	ACCESSION VERSION KEYWORDS SOURCE	RESULT 11 AE016767/c LOCUS DEFINITION	Db 349	ω	Db 350	tu.	Lui	i.i.	1.3	Q B
/locus tag="63796" /note="Bscherichia coli K-12 ortholog: b3042; Escherichia coli O157:H7 ortholog: z4400"	/10cus tag="c3796" /10cus tag="c3796" 188547 /gene="yq1C"	/strain="CFT073" /db_xref="taxon:199310" 18B547 /gene="yor(C"	Location/Qualifiers 1. 300359 /organism="Escherichia coli CFT073" /mol type="genomic DNA"	Perna,N.T., Mobley,H.L.T., Donnenberg,M.S. and Blattner,F.R. Direct Submission Submitted (20-JUN-2002) Genetics Laboratory, University of Wisconsin - Mailson, 445 Henry Mall. Madison, WI 53706, USA	2 (bases 1 to 300359) Welch, R.A., Burland, V., Plunkett, G.D. III, Redford, P., Roesch, P., Rasko, D.A., Buckles, E.L., Liou, SR., Boutin, A., Hackett, J., Stroud, D., Mayhew, G.F., Rose, D.J., Zhou, S., Schwartz, D.C.,	Extensive Mosiac Structure Revealed by the Complete Genome Sequence of Uropathogenic Escherichia coli Proc. Natl. Acad. Sci. U.S.A. 99 (26), 17020-17024 (2002) 12471157	elch,R.A., Bur asko,D.A., Buc troud,D., Mayh	<pre>Becherichia coli CFT073 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia. 1 (bases 1 to 300359)</pre>		AB016767 300359 bp DNA linear BCT 24-DEC-2002 Recherichia coli CFT073 section 13 of 18 of the complete genome.				UCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC			AAAGTGGTAATGACCAAGGTGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCCTCCACC	1932 GGCGTGATGACCGAAGAGGAACTGAAGCTGGCTGTAGTGGCAGCGCGTAAACGTGGTGAA 35282 1921 AAAGTGGTGATGACCAACGGTGTGTTTTTGACATCCTGACGACGCCGGGCACGTCTCTTATCTG 1980

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TVGGVQNTVAEDLSKNGLELESVSLTNFNQTSKEHFNPNNAFDAEGLTKLTQETERRR
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                                                     complement (3788.
                                                                                                     complement (3788.
                                                                                                                           SAALSYRTQAPLIDSLLNEIGVSGSLAALTSSLSSTTPVBEKAB"
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/note="Escherichia coli K-12 ortholog: b3050; Escherichia
coli O157:H7 ortholog: z4402"
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protein_id="AAN82244.1"
db_xref="GI:26110058"
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ETLIVAARDHIYDACCREWGTPCNAGGEAQPILIILGWGKLGGGELNPSSDIDLIFAWP
EHGCTQGGBRELDNAQFTPBMGQRLIKVLDQPTQDGFVYRUDMRLRPFGESGFLVLSF
AALEDYYQBQGRDWERYAWVKARIMGDSDGVYANELRAMLRPFVFRRYIDFSVIQSLR
NMKGWIAREVRRRGLITDNIKLGAGGIRBIBFIVQVFQLIRGGREPSLJQSRALLFTLSA
IAALHLLSENDAEQLRVAYLFLRRLENLLQSINDEQTQTLPFDELNRARLAWAMDFAD
WPDLTGVLTAHMANVRRVFNELIGIDESETQBESLSBQWRELWODALQBDTTFVLAH
LSEDDRKQVLMLIADFRKELDKRTIGBPGRGVUDHLMPHLLSDVCAREDAAVTLSRIT
ALLVGIVTRTTYLELLSBFPAALKHLISLCCASFMIASQLARYFLLLDBKLDFWTLYQ
PTATDAYRDELRQYLLRVPEDDBEGQLEALRQFKQAQLLRIAAADIAGTLFVMKVSDH
LTFLHBCFWDAWTGWTARYGKENHLMEREGRGFVKVGYGKLGGWELGYSSDLD
LIFLHBCFWDAWTDGERSIOGRGFVLRAGNIMHLFSTRTSGGILFVTDARLARFGGAA
GMLVTSAEAFADYQKNEAWTWEHQALVRARVVGTGDPQLTAHFDAVRREIMTLPREGKT
LQTTVFREMERWRAHLGNKHRDRFDIKADEGGITDLEFITQYLVLRKAHEKFKLTRWS
LTGTHBCHMAMTDGERSIOGRGKHRDRFDIKADEGGITDLEFITQYLVLRKAHEKFKLTRWS
LGTTYTSAEAFADYQKNEAWTWEHQALVRARVVYGDPQLTAHFDAVRREIMTLPREGKT
LQTTVFREMERWRAHLGNKHRDRFDIKADEGGITDLEFITQYLVLRKAHEKFKLTRWS
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GNSLEBACFFANAAGVVVGKLGTSTVSPIELENAVKGRADTGETGVMTEEELKLAVAA
ARKRGEKVMTNGVFDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDSRFVND
LBQRMIVLGALEAVDMVVSFEEDTPQRLIAGILPDLLVKGGDYKPEBIAGSKEVWANG
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                                                                                              GYYDPVVAQDWLENWQGLRHAIATGQRIBIBHFRNBANNQBPFWLHSGKR"
                                                                                                                                                                         /translation="MGGVPSGGRMAQBIELKFIVNHSAVEALRDHLNTLGGEHHDPVQ
LLNIYYETPDNWLEGHDMGLRIRGENGRYENTMKVAGRVTGGLHQRPSYNVALSEPTL
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PARPICELELELLSGDMRAVLKLANQDLVSQTGLRQGSLSKAARGYHLAQGNPAREIK
TTILHVAAKADVEQSLEAALELALAQWQYHBELWVXGNDAAKEQVLAAIGLVRHTLML
FGGIVPRKASTHLRDLLTQCEATIASAVSAVTAVYSTETAMAKLALTEWLVSKAWQPP
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modification"
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coli 0157:H7 ortholog: z4405"
                                                               complement (9503
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complement(8132. .9460)
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lqqywqtvverlpeplaeeslsaqaksvltpsdfvqdsvlahpewltblesqppqade
wqhyaswlqbalsnvsdeaglmrelrlprrrimvriawaqtlalvtbesilqqlshla
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/protein_id="AAN82245.1"
                                                                                                                                              LDAKAQSKISDSFKRFADIHLSRHAAELKSVFCQPLGDRYRDQLPRLTRDIDSILLLA
                                                                                                                                                                                                                                                                                                                                                                                                       product="Hypothetical
protein_id="AAN82247.;
/db_xref="GI:26110061"
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/note="ORFXE; Escherichia coli K-12 ortholog: b3054;
/scherichia_coli O157:H7 ortholog: z4407"
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db_xref="GI:26110060"
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EC_number="2.7.7.42"
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db_xref="GI;26110059"
tag="c3803"
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   GGTGCGGGCGACACGGTGATTGGCGTCCTGGCGGCAACGCTGGCAGCGGGTAATTCGCTG
                                                                GCCGATTACGAACTCTCGGCTCTGTTAGTGACCCCGTTCCGAACAGGGTATGTCGCTGCTG
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/trans[table=11
/product="putative Transposase"
/protein_id="AAN82248.1"
/db_xref="G1:26110662"
/td_xref="G1:26110662"
/td_xref="G1:26110662"
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TSRRLRNDFIDLRAAYSKPVLWSRSYFIGSCGGAPLEVVKKYIQNQRG"
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/function="putative enzyme; Transposases"
/note="Escherichia coli O157:H7 ortholog: z5815"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4441 GGTGCGGGCGACACGGTGATTGGCGTCCTGGCGGCAACGCTGGCAGCGGGTAATTCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    901
                                                                                                                                                                                                                                                                                                                                            genome.
AE016988
AE016988.
                                                                                                                                                                                                                                                                                                                                                                                       AE016988
Shigella
Direct Submission
Submitted (13-JUN-2002) Genetics Laboratory, University of
Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
                                                                                                                                                   Wei,J., Goldberg,M.B., Burland,V., Venkatesan,M.M., De Fournier,G., Mayhew,G.F., Plunkett,G. III, Rose,D.J., Mau,B., Perna,N.T., Payne,S.M., Runyen-Janecky,L.J., 2 Schwartz,D.C. and Blattner,F.R. Complete Genome Sequence and Comparative Genomics of Selexneri Serotype 2a Strain 2457 Infect Immun. 71 (5), 2775-2786 (2003)
                                                                                                                                                                                                                                                   Shigella flexneri 2a str. 2457T
Shigella flexneri 2a str. 2457T
Shigella flexneri 2a str. 2457T
Bacteria, Proteobacteria;
Enterobacteriaceae; Shigella.

1 (bases 1 to 292906)
Wei I Collabera M B Burland V Venkaragan N
                                                           2 (bases 1 to 292906)

Wei,J., Goldberg,M.B., Burland,V., Venkatesan,M.M., Deng,W.,
Fournier,G., Mayhew,G.F., Flunkett,G. III, Rose,D.J., Darling,A.,
Mau,B., Perna,N.T., Payne,S.M., Runyen-Janecky,L.J., Zhou,S.,
Schwartz,D.C. and Blattner,F.R.
                                                                                                                                      12704152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGTGGTGATGACCAACGGTGTCTTTGACATCCTGCACGCCGGGCACGTCTCTTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGAAGCCTGCTTCTTTGCCAATGCGGCGGCTGGTGGTGGTCGGCAAACTGGGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGAAGCCTGCTTCTTTGCCAATGCGGCGGCTGGCGTGGTGGTCGGCAAACTGGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTTGCTCGACGACCAACATCATCAAGAAGATCCAACTGGATAAAAAAAGGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTTGCTCGACGACCAACATCATCAAGAAGATCCAACAGGATAAAAAAGGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCGCCGGGATCTTGCCAGATCTGCTGGTGAAAGGCGGCGACTATAAACCAGAAGAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAGAGGGCCACGCCGCAGCGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACGGCTGAAAGGGGATTCCCGCCCGGTAAACCCCACTCGAACAGCGTATGATTGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAAATGCCCGTAAACTGGGTGACCGTTTGATTGTCGCTGTGAACAGCGATGCCTCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAAATGCCCGCAAGCTGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCCTCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGTGATGACCGAAGAGGAACTTGAAGCTGGCCGTAGCGGCAGCGCGTAAACGTGGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCACGGTTTCGCCGATCGAGCTGGAAAAACGCAGTACGTGGACGTGCAGATACCGGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCACGGTTTCGCCGATCGAGCTGGAAAATGCTGTACGTGGACGTGCAGATACAGGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGCTGGTGCTCAACTTTGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCGCCGGGATCTTGCCAGATCTGCTGGTGAAAGGCGGCGACTATAAACCAGAAGAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGCACTGGAAGCGGTCGACTGGGTGGTGTCGTTTGAAGAGGACACGCCGCAGCGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACGGCTGAAAGGGGATTCCCGCCCCCGTTAACCCCGCTCGAACAGCGTATGATTGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAGTGGTGATGACCAACGGTGTCTTTGACATCCTGCACGCCGGGCACGTCTCTTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGTGATGACCGAAGAGGAACTGAAGCTTGCTGTAGCGGCAGCGCGTAAACGCGGTGAA
                                                                                                                                                                                                                                                                                                                                             AE014073
.1 GI:30042420
                                                                                                                                                                                                                                                                                                                                                                                          flexneri
                                                                                                                                                                                                                                                                                                                                                                                          2a
                                                                                                                                                                                                                                                                                                                                                                                        292906 bp
a str. 2457T
                                                                                                                                                                                                                                                                                                                                                                                          DNA
section
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H

linear of 16 of

22-APR-2003 complete

1434

3842

1380

3902

1320

3962

1260

4082 1140

1200

4142 1080 4202 1020 4262

4022

Enterobacteriales;

of Shigella

Deng, W., ., Darling, A.

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gene
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                                                                                                                                                                                                                                        883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gg
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                                                                                                                                                                                              ruccus_tag="83032"
complement(3835. .4200)
/gene="ygdB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus tag="S3031"
/function="putative enzyme; Not classified"
/note="residues 1 to 116 of 116 are 81.03 pct identical to
residues 1 to 107 of 107 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RQSYAREMLPAASQAGKAHSERVQPLPFTLPETVPLETLQRFWAHFVAAPFQMRLQVN
FHTEDSEIPDTEPFILEGLER FQINQQLLANLYUZQDDARRLFRAFRAAGDLPYGAGE
IFWETQCQBMQQLANBYIACRQPGQSWEIDLACKNGVQITGMLPQVQPDGLLRWRPSEL
SVAQGMQLWLEHLYYCASGGNGESRLFLRKDGEWRFPPLAAEQALHYLSQLIEGYREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAQYGDAVPLSLLRDELAQRLDQBRISQRFLAGPVNICTLMPMRSIPFKVVCLLGMND
GVYPRQLAPLGFDLMSQKPKRGDRSRRDDDRYLFLBALISAQQKLYISYIGRSIQDNS
BRFPSVLVQBLIDYIGQSHYLPGDBALNCDBSBARVKAHLTCLHTRMPFDPQNYQPGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEAF I SLLSLPDSRFVSEDVLALLDVPVLAARFD I TEEGLRYLRQWVNESGI RWGI DD
DNVRELELPATGQHTWRFGL TRMLLGYAMESAQGEWQSVLPYDESSGL I AELVGHLAS
LLWQLN I WRRGLAQERPLEEWLPVCRDMLNAFFLPDAETEAAWTL I EQQWQA I I AEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WLQMTLSQKFGIAANIDFPLPASFIWDMFVRVLPEIPKESAFNKQSMSWKLMTLLFQL
LEREDFTLLRHYLTDDSDKRKLFQLSSKAADLFDQYLVYRPDWLAQWETGHLVEGLGE
AQAWQAPLWKALVEYTHBLGQPRWHRANLYQRFIBTLESATTCPPGLPSRVFICGISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="DNA helicase, ATP-dependent dsDNA/ssDNA
exonuclease V subunit, ssDNA endonuclease"
/transl_table=11
/product="hypothetical_protein"
/protein_id="AAP18147.1"
                                                                                                                                                                                                                                                                                                         complement (3835. .4200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (3500. .3850)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSAPLLVLPESGGAWLKTCYDAQNDAMLDDDSTLQKARTKFLQAYEGNMYVRGEGDDI
WYQRLWRQLTPETMETIVEQSQRPLLPLFRFNQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPPVYLQALQALGKHI BIHLLFTNPCRYYWGDIKDPAYLAKLLTRQRRHSPEDRBLPL
FRDSENAGQLFNSOEGQDVGNSLLASWGKLGRDYI YLLSDLESSQGELDAFVDVTPDNL
LHNIQSDILELENRAVAGNYI EEFBRSDNKRPLDFLDSSI TFHVCHSPQAFAVEVLHD
LLAMLEEAPTLTPRDI I VMVADI DSYSPFIQAVFGSAPADRYLPYAI SDRRARQSHPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="83030"
complement(119. .3487)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .292906
                                                                                                                                                                                                                                                                                                                                      rsmnslasrnqyqqlwrhgwqqtqlraisppanwqvnrmqtsqagcvsisvtlvspgg
Regemtrlhcpncq"
                                                                                                                                                                                                                                                                                                                                                                                                                            /transT table=11

product="prepilin peptidase dependent protein protein id="AAP18146.1"
                                                                                                                               note="residues 16 to residues 16 to 121
                                                                                                                                                                                                                                                                                  gene="ygdB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene≖"ppdC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /funct-Ion="enzyme; Degradation of DNA"
note="residues 1 to 1122 of 1122 are 96.34 pct identical
o residues 1 to 1122 of 1122 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Shigella flexneri"
| mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MLRVYHSNRLDVLEALMEFIVERERLDDPFEPEMILVQSTGMAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:198215"
complement(119. .3487)
                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                     translation="MSASLKNQQGFSLPEVMVAMVLMVLMVLMVLMVMIVTALSGIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serotype="2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="genomic
strain="2457T"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocus_tag="83030"
                                                                                                                                                                                                                                                                                                                                                                                                                 xref="GI:30042422"
                                                                                                                                                                                      tag="83032"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tag="83031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (3500. .3850)
                                                                                                                                     o 121 of
1 of 121
                                                                                                                                     121 are 96.22 pct identical from Escherichia coli K-12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2a str. 2457T"
                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SgS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SdC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                 complement (7274.
                                                            MMVWAYRRSPQQHVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="thyA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="GI:30042423"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="lgt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="ppdA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            locus_tag="S3036"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      locus_tag="S3035"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocus_tag="S3034"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tag="83036"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tag="83033"
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complement (6248. .7123)
/gene="lgt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQLYQRSCDVFLGLPFNIASYALLVHMMAQQCDLEVGDFVWTGGDTHLYSNHMDQTHL
QLSREPRPLPKLIIKRKPESIFDYRFEDFEIEGYDPHPGVKAPVAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="milvigsliliqqmsqqdrsfasrvsmesqsirrqaivqsalawg
kmhswqrqpavqcsqyagrdaqvclriladnealliagyegvslwrrgevidgkivfs
prgwsdfcplkegalcqlp"
                               HGGLIGVIVVMIIFARRTKRSFFQVSDFIAPLIPFGLGAGRLGNFINGELWGRVDPNE
PFAMLFPGSRTEDILLLQTNPQWQSIFDTYGVLPRHPSQLYELLLEGVVLFIILNLYI.
                                                                                             /db_xref="G1:30042426"
/translation="MTSSYLHFPEFDPVIFSIGPVALHWYGLMYLVGFIFAMMLATRR
ANRPGSGWTKNEVENLLYAGFLGVFLGGRIGYVLFYNFPQFWADPLYLFRVWDGGMSF
                                                                                                                                                                                                                                                                                                                                                                                           /note="residues 1 to
residues 1 to 291 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="enzyme; Macromolecule synthesis, modification:
Phospholipids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (5447. .6241)
/gene="thyA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVNMRAASKSEPQTVVDASYSVTGFNL"
complement (4793. .5263)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /locus_tag="S3033"
complement (4239. .4802)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (4239. .4802)
RKPRPMGAVSGLFLIGYGAFRIIVEFFRQPDAQFTGAWVQYISMGQILSIPMIVAGVI
                                                                                                                                                                                          /codon start=1
/crans[ table=1]
/product="phosphatidylglycerol-prolipoprotein
/product=thosphatidylglycerol-prolipoprotein
/protein_id="AAP18150.1"
/protein_id="AAP18150.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKQYLELMQKVLDEGTQKNDRTGTGTLSIFGHQMRFNLQDGFPL
VTTKRCHLRSIIHELLWFLQGDTNIAYLHENNVTIWDEWADENGDLGPVYGKQWRAWP
IPDGRHIDQITTVLNQLKNDPDSRRIIVSAWNVGELDKWALAPCHAFFQPYVADGKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon start=1
'transT_table=11
'product="thymidylate synthetase"
'product="tA-"nAP18149.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /locus tag="S3035"
/function="enzyme; 2-Deoxyribonucleotide metabolism"
/function="enzyme; 2-Deoxyribonucleotide metabolism"
/note="residues 1 to 264 of 264 from Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LALEDEIWLRVFTVAKHLQRAGYCHGSCTGEGLEIVGQGDCIIVQWDANSNGIWDREP
VKESDQIGFRLKEHVLETLRGATSCEGKGWDKVTNPDAIIIDTFQVVRQDVSGFSPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               producE="prepilin peptidase dependent protein
/protein_id="AAP18148.1"
/db_xref="GI:30042424"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (6248. .7123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAP18149.
db_xref="GI:30042425"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'functTon="putative enzyme; Not classified" note="residues 1 to 187 of 187 are 98.39 pct esidues 1 to 187 of 187 from Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="point mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MPVKEQGFSLLEVLIAMAISSVLLLGAARFLPALQRESLTSTRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ıplement (5447. .6241)
                                                                                                                                                                                                                                                                                                                                                                                           291 of 291 are 95.87 pct identical to 291 from Escherichia coli K-12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identical to i K-12:
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complement(7274. .9520)
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                                                                                                                                                                                                                                                    ATCGCCGGGATCTTGCCAGATCTGCTGGTGAAAGGCGGCGACTATAAACCAGAAGAGATT
                                                                                                                                                                                                                                                                                                                                                    GGCGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAGAGGACACGCCGCAGCGCTTG
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GGCTGCTCAACTACCAATATTATTAAGAAAATACAAAAAGATA
                                                                                                        GCCGGCAGCGAAGAGGTCTGGGCGAACGGTGGCGAAGTGCTGGTGCTCAACTTTGAAGAT
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                                                                                                                                                                                                                                                                                                                        GGGGCGCTGGAAGCGGTCGACTGGGTGGTATCATTTGAAGAAGATACTCCGCAGCGCCTG
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AL627278

AL627278

AL627278

CON AL627278 AL513382

AL627278.1 GI:16504263

Salmonella enterica subsp. enterica serovar Typhi
ISM Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteria; Bacteria; Dougan, G., James, K.D., Thomson, N.R., Pickard, D.,
RS Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D.,
RS Parkhill, J., Churcher, C., Mungall, K.D., Bentley, S.D., Holden, M.T.,
Sebaihia, M., Baker, S., Basham, D., Brooke, K., Chillingworth, T.,
Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N.,
Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S.,
Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P.,
Parry, C., Quall, M., Rutherford, K., Simonds, M., Skelton, J.,
Stevens, K., Whitehead, S. and Barrell, B.G.
Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18
AL Nature 413 (6858), 848-852 (2001)
RC Complete Submission
RC Sarkhill, J.
Sirect Submission
Sirect Submission
Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing campus, Hinxton, Cambridge CB10 1SA, UK
E-mail: parkhill@sanger.ac.uk

gene

Sg

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PEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/S_typhi/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tranel tet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="UniProt/Trembl:QBXGZ1"
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/db_xref="UnterPro:IPR010130"
/db_xref="InterPro:IPR010130"
/db_xref="InterPro:IPR010130"
/db_xref="InterPro:IPR010130"
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/db_xref="InterPro:IPR010130"
/db_xref="InterPro:IPR010130"
/db_xref="UnterPro:IPR010130"
/db_xr
Orthologue of E. coli ygiC (YGIC_ECOLI); Pasta hit to YGIC_ECOLI (386 aa), 94% identity in 386 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                               /note="PS00013 Pattachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Orthologue of E. coli ygiB (YGIB_ECOLI); Fasta hit
to YGIB_ECOLI (234 aa), 97% identity in 223 aa overlap.
Contains a possible N-terminal signal sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLNVEHFKTDKFKAVNALLKEAENRNLSLLQARLSQDLAREQIRQAQDGHLFTLNLTA
STGISDTSYBGBKTNSAQYDDSNMGQNKIGLNFSLFLYQGGMVNSQVKQAQYNFVGAS
EQLESAHRSVVQTVRSSFNNINASISSINAYKQAVVSAQSSLDAMEAGYSVGTRTIVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aa) fasta scores: E(): 0, 89.7% id in 495 aa Orthologue of E. coli tolC (TOLC_ECOLI); Fasta hit to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1835.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |935. .1867
|gene="STY3365"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="possible lipoprotein"
protein_id="CAD07713.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /ldatttlydakqqlanarytylinqlnikyalgtlneqdllalnstlgkpiptspes
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protein_id="CAD07712.1"
                                                                                                                                                                                                                  'gene="STY3366"
                                                                                                                                                                                                                                                                                                                   'gene="STY3366"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:90370"
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strain="CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Salmonella enterica subsp. enterica serovar
                                                                                                                                                 note="Fasta hit to YJFC_ECOLI (387 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="STY3365"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _xref="GI:16504265"
                                                                                                           aa overlap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECOLI (495 aa), 90% identity in 495 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prokaryotic membrane lipoprotein lipid
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                                                                                                                                                      50% identity in
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FTDLQDQVIANLFKLYPWEFMLREMFSTKLEDAGVRWLEPANKSIISNKÄLLPLLMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSIKRTAILLTLGISLHNPPEGIATFVTASSNLELGFGIALAVALHNIPPEGLAVÄGPV
YAATGSKRTAIFWAGISGWABILGGVLAWLILGSLVSPIVMAAIMAAVAGIMVALSVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Orthologue of E.'coli ygiE (YGIE ECOLI); Fasta hit to YGIE_ECOLI (257 aa), 93% identity in 257 aa overlap. Contains multiple possible membrane spanning hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQRLVELLAFVPVALDKEAMGFDHGSWGVLIKÑYPNADIPMVÕLSVDSTKPAAMHFEM
GRKLATLRDEGVMLVASGNVVHNLRTVRWHGDNIPYFWAASFNDFVKANLTWQGPVEQ
HPLVNYLQHEGGALSNPTPEHFLPLLYVLGAWDGKEPITIPVDGIEMGSISMLSVQVG
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/gene="STY3367"
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/gene="STY3367"
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VQQPYPLPKFGDSYTLIGSWLINDQPAGIGIREDRALITQDLSRFYPHIFVEG"
DPYGNAPLTALVELDSHI I SDVKVTVHGKGEKGVPVTYTVGKESLETYDGI PI FGLYQ
KFANNVTVEYKENGKAMKDDYVVQTSA I VNHYMDNRS I SDLQQTKV I KVAPGFEDRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLMPLAKBIDPNNNPSYGVLCGMSIMGLSLVILQTIGIG"
                                                                                                                                                                                                                                                                                                                                                /note="Similar to Klebsiella pneumoniae arylsulfate
sulfotransferase assT TR:P97036 (EMBL:U32616) (598 a
fasta scores: E(): 0, 86.8% id in 598 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5004. .7B00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLISLMEMLPAALDTEGMSPVLGYGMFIIGLLGYFGLDRLLPHAHPQDLVQKRQQPLP
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                                                                                                                                                          db_xref="GOA:Q8Z3N6"
                                                                                                                                                                                                                                                                                       codon_start=1
transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="STY3370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="synonym: assT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="STY3370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="GOA: P67471"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="STY3368"
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db_xref="GI:16504267"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="conserved hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="conserved hypothetical protein
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                                                                                                                                                                                                                                                     arylsulfate sulfotransferase"
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Matches 1164;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGCTGAGCAAAACGCTGGCGGAGGTCAATGTGAAGTGCGACTTCGTTTCTGTGCCGACG
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                              GCTGTTGTCGGTAAATGTAAGACCGAAGAAGAGATTGTTGAGCGCGGCATGAAACTGATT 660
                                                                                        ACGGATTTTGAACGTTACCGCGCGCCCACGCTGCTGACGCCAAACCTTTCTGAATTTCGAG 14894
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  GCGGTTGCGGGGAAATGTAAAAGCGAAGACGAACTGGTTGAACGCGGCATGAAGCTCATT
                                                                                                                    ACCGATTTTGAGCGCTACCGCGGCGCTACGCTGTTAACGCCGAATCTCTCGGAATTTTGAA 600
                                                                                                                                                                              CAGACTATGATTTCCCTAGCGCGCCCAGGCGGGCGTGCCGGTGCTCATCGATCCGAAAGGA
                                                                                                                                                                                                                        CTGGGATCGATCGCGCTGGTATTGTCCGATTATGCCAAAGGCGCTCTGACCAGCGTG
                                                                                                                                                                                                                                                                                                                 CTGAGTTCGATTGGCGCGCTGGTGCTTTCTGACTACGCCAAAGGTGCGCCTGGCAAGCGTA 480
                                                                                                                                                                                                                                                                                                                                                                                                     TTTGAAGAAGGTTTCGAAGGTGTTGATCCGCAGCCGCTGCACGAGCGGATTAATCAGGCG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATCCGACGATTACCAAACTGCGCGTACTATCACGTAATCAGCAGCTCATTCGTCTTGAT 15134
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ASHESIETVNGTYLLRVGKRDYRKEDGJHYFIT RDQIIEVDKGCYUDVMDLTKILDP
MRDALLGALDAGAVCYNVDLAHAGQDAKLEPDTFYGDALEVDKGGRNMAHVNSIAYDAK
DDSIILSSRHQGIVKIGRDKQVKWILAPSKGMNKQLASKLLKPVDDHGKPLTCDENGK
CKDTDFDFTYTQHTAMLSKGTLTVFDNGDGRGLEQPALFTMKYSRFVBYKIDEKKGT
VQQVWEYGKREGYDFYSFJTSVVEYQKDRDTWGFGFGGSINLFDVGKFTVGKLNEIDYK
TKGVKVEIDVLSDKPNQTHYRALLVHFTQMFK**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="dsbA"
/note="Similar to Enterobacter amnigenus disulfide
isomerase dsbA TR:(99XDP1 (EMBL:AF012826) (222 aa) i
scores: E(): 0, 90.1* id in 222 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="dsbA"
/note="synonym:
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81.8%;
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Pred. No. 3.5e-225;
0; Mismatches 259;
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8	14833	
Ş	721	CAACCGGGTAAAGCGCCGCTGCATATGCCAACCCAAGCGCAGGAAGTGTATGACGTTACC 780
용	14773	CAACCGAATAAAGCGCCGCTACATATGCCGACGCAGGCGCAGGAAGTTTATGATGTTACC 14714
Ş	781	GGTGCGGCGACACGGTGATTGGCGTCCTGGCGGCAACGCTGGCAGCGGGTAATTCGCTG 840
용	14713	GGTGCGGGCGATACGGTGATCGGCGTGCTGGCGGCGACGCTGGCGGCGAAAATACCCTG 14654
Ş	841	GAAGAAGCCTGCTTTTGCCAATGCGGCGGCTGGCGTGGTGGTCGGCAAACTGGGAACC 900
용	14653	GAGGAGGCGTGTTATTTCGCCAATGCGGCGGCGGCGGTAGTTGGTAGGTA
Ş	901	TCCACGGTTTCGCCGATCGAGCTGGAAAATGCTGTACGTGGACGTGCAGATACAGGCTTT 960
용	14593	TCAACGGTTTCCCCTATTGAGCTGGAAAACGCAGTGCGCGGACGCGGGATACCGGCTTC 14534
δ	961	GGCGTGATGACCGAAGAGGAACTGAAGCTGGACGTGGCGGAGCGCGTAAACGTGGTGAA 1020
용	14533	GGCGTCATGACCGAAGAGGGGTTGAGACAGGCCGTCGCCAGCGCGTAAGCGTGGCGAG 14474
Ş	1021	AAAGTGGTGATGACCAACGGTGTCTTTGACATCCTGCACGCCGGGCACGTCTCTTATCTG 1080
문	14473	ANAGTGGTCATGACCAACGGCGTTTTCGATATTCTGCACGCGGGCCACGTCTCTTATCTG 14414
Ş	1081	GCAAATGCCCGCAAGCTGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCCTCCACC 1140
용	14413	GCGAACGCGCGCAAACTGGGCGACCGCCTGATTGTTGCGGTCAATAGTGACGCCTCGACT 14354
Ş	1141	AAACGGCTGAAAGGGGATTCCCCGCCCGGTAAACCCCACTCGAACAGCCGTATGATTGTTGCTG 1200
몽	14353	AAACGTCTGAAAGGCGAAAAGCCGTCCGGTTAATCCGCTCGAACAGCGTATGATCGTGCTG 14294
δ	1201	GGCGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAGAGGACACGCCGCAGCGCTTG 1260
문	14293	GGCGCGCTGGAGTCGGTCGACTGGGTTGTCTCTTTTGAAGAGGATACGCCGCAACGACTG 14234
δ	1261	ATCGCCGGGATCTTGCCAGATCTGCTGGTGAAAGGCCGGCGACTATAAACCAGAAGAGATT 1320
용	14233	ATTGCCGGTATTCTGCCGGATCTGCTGGTAAAAGGCGGCGACTATAAGCCGGAAGAGATC 14174
δ	1321	GCCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGAC 1380
문	14173	CCGGCCAGCGAAGAGGTCTGGGCCCAACGGCGGCGAAGTCATGGTGCTGAACTTCGAAGAT 14114
Ş	1381	GGTTGCTCGACGACCAACATCAACAGAAGATCCAACAGGATA 1423
7	14111	CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE

Search completed: March 18, 2006, 21:59:53 Job time : 7130 secs

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GCCGATTACGAACTCTCGGCTCTGTTAGTGACCCCGTTCCGAACAGGGTATGTCGCTGCTG 720

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                   Published Applications NA New:*

1: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

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  100.0 1434 8 US-10-520-820-28
18.1 377 9 US-11-116-881A-1812
17.7 960 8 US-10-467-657-3253
7.5 507 8 US-10-467-657-3253
7.5 507 8 US-11-098-686-8739
4.4 1038 12 US-11-098-686-8739
4.4 1038 12 US-11-098-686-8739
3.6 12 US-11-098-686-6509
3.0 3477 8 US-11-098-686-4509
3.0 3477 8 US-11-098-688-31210
2.6 2539 US-11-096-568A-31210
2.6 2539 US-11-096-568A-31287
2.6 88421 12 US-11-096-568A-31287
2.6 89821 12 US-11-096-568A-31287
2.6 3513 US-10-467-657-7053
2.6 3513 US-10-467-657-7084
2.4 1412 9 US-11-096-568A-26296
2.4 200 12 US-11-096-568A-26296
2.4 1412 9 US-11-096-568A-26296
2.4 1412 9 US-11-096-568A-26296
2.4 1412 9 US-11-096-568A-26296
2.4 1412 9 US-11-096-568A-6279
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Match Length DB ID
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Gapop 10.0 , Gapext 1.0
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1434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8023312 seqs, 1165852854 residues
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Sequence 28, Appl
Sequence 1812, Ap
Sequence 3253, Ap
Sequence 547, App
Sequence 8739, Ap
Sequence 8739, Ap
Sequence 6509, Ap
Sequence 141, App
Sequence 31210, A
Sequence 31210, A
Sequence 31210, A
Sequence 31087, Ap
Sequence 7053, Ap
Sequence 7053, Ap
Sequence 7053, Ap
Sequence 7053, Ap
Sequence 1145, Ap
Sequence 2636, A
Sequence 10264, A
Sequence 10264, A
Sequence 4617, Ap
Sequence 4617, Ap
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32.4	32.4	32.4	32.4	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.8	32.8	32.8	33	33	33	33.2	33.2	33.4	33.4	33.4	33.4	33.6
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Sequence 16, Appl Sequence 36, Appl	Sequence 14, Appl	Sequence 14, Appl	Sequence 3275, Ap	Sequence 13274, A	Sequence 5041, Ap		Sequence 20738, A	Sequence 23715, A	Sequence 5, Appli	Sequence 14, Appl	Sequence 1278, Ap	Sequence 12361, A	Sequence 2265, Ap	Sequence 539, App	Sequence 17, Appl	Sequence 17, Appl	Sequence 13367, A	Sequence 4, Appli	Sequence 42527, A	Sequence 42527, A	Sequence 12879, A	Sequence 6513, Ap	Sequence 1544, Ap

ALIGNMENTS

B 8	B 8	B &	B &	Query Match Best Local Si Matches 1434;	; NUMBER OF SEQ ; SOPTWARE: PAT SEQ ID NO 28 ; SEQ ID NO 28 ; LENGTH: 1434 ; TYPE: DNA ; TYPE: DNA ; ORGANISM: E8 US-10-520-820-28	FILE RE CURRENT CURRENT PRIOR A PRIOR F PRIOR A PRIOR A PRIOR F	RESULT 1 US-10-520-820-28 Sequence 28, App. Sequence 28, Information No. GENERAL INFORMATION INTERVENT. TITLE OF INVENTITLE OF
181 GCTTCTCTCGGTGCTAATGCACGCC	121 GTTAAAGTGAATACCAT	61 CTGGATCGTTACTGGTA	1 ATGAAAGTAACGCTGCC 1 ATGAAAGTAACGCTGCC	/ Match 100.0%; Local Similarity 100.0%; nes 1434; Conservative	UMBER OF SEQ ID NOS: 32 OFFWARE: PATENTIN VERSION 3.1 Q ID NO 28 LENGTH: 1434 TYPE: DNA ORGANISM: Escherichia coli 0-520-820-28	RENCE: 1621 PPLICATION NUMBER: PLING DATE: 2005- LLICATION NUMBER: PING DATE: 2003-07- LICATION NUMBER: PLICATION NUMBER	pplicat . US200 ATION: TABILIS TABILIS NTION: NTION:
GCTTCTCTCGGTGCTAATGCACGCCTGGTCGGGTTGACGGGCATTGACGATGCAGCGCGC 	GTTAAAGTGAATACCATCGAAGAACGTCCGGGCGGCGGCGGCTAACGTGGCGATGAATATC	CTGGATCGTTACTGGTACGGCCCCACCAGTCGTATCTCGCCGGAAGCGCCGGTGCCCGTG	atgaaagtaacgctgccagagtttgaacgtgcaggagtgatggtggttggt	Score 1434; DB 8; Pred. No. 0; 0; Mismatches 0;	į.	US/10/520,820 01-07 CT/BP2003/008209 R 0208636	eterminants which enting and control
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2300
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1812
LENGTH: 377
TYPE: DNA
ROGANISM: Nicotiana tabacum
US-11-116-881A-1812
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PRIOR FILING DATE: 2005-03-24
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PRIOR PELING DATE: 2005-01-25
PRIOR PILING DATE: 2005-01-25
PRIOR PILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/566,235
PRIOR FILING DATE: 2004-09-03
PRIOR FILING DATE: 2004-09-03
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2004-09-13
PRIOR PRIOR DATE: 2004-09-17
PRIOR PILING DATE: 2004-09-17
PRIOR PILING DATE: 2004-09-17
PRIOR PILING DATE: 2003-09-18
PRIOR PILING DATE: 2003-09-18
PRIOR PILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: 60/485,368
PRIOR PILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: 60/485,368
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PRIOR PRILING DATE: 2003-07-08
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TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules
FILE REFERENCE: 07678/141014
CURRENT APPLICATION NUMBER: US/11/116,881A
CURRENT FILING DATE: 2005-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: 60/418,933
PRIOR FILING DATE: 2002-10-16
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  CAACAGGATAAAAAAAGGCTAA
                                                                              GAAGTGTTGGTGCTCAACTTTGATGACGGTTGCTCGACGACCAACATCATCAAGAAGATC
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Pred. No. 3.6e-70;
0; Mismatches 1
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Best Local Similarity
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ORGANISM: Neisseria gonorrhoeae
;-10-467-657-3253
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LENGTH: 960
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
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APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Eliasbetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND
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SOFTWARE: SegWin99, version 1.04
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ACCGAAGAAGAGACTCTTGAGCGCGGCATGAAACTGATTGCCGATTACGAACTCTCGGCT 681
                                                                             GGCGCTACGCTGTTAACGCCGAATCTCTCGGAATTTGAAGCTGTTGTCGGTAAATGTAAG
                                                                                                                            AAACATGTCGGCAAAACCGTCTTAATCGACCCCAAAGGCGACGATTACGAAAAATATGTC
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                                                                                                                                                                    CGTAAAGCGGGTGTTCCGGTGCTGATTGATCCAAAAGGTACCGATTTTGAGCGCTACCGC
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PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SegWin99, version 1.04
SEQ ID NO 547
LENGTH: 507
TYPE: DNA
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-547
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US-10-467-657-547
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Publication No. US20050260581A1
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APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
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CURRENT FILING DATE: 2003-08-11
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                                     CCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGACG 1381
                                                                                                             TCGCCGGGATCTTGCCAGATCTGCTGGTGAAAGGCGGCGACTATAAACCAGAAGAGATTG 1321
                                                                                                                                                                                              GCGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAGAGACACGCCGCCGCAGCGCTTGA
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TCGGTGCGGCGGAAACGCTGGCACGCGGCGGTCAGGTGTTTTTCAATTCCGTTTCTGCATC
                                                                                                                                                                 CCGCGTTGGAAAGTGTGGATTTGGTTACTTGGTTTGACGAGGATACGCCGGCGGCGTTGA
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Conservative
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Pred. No. 3e-23;
0; Mismatches 168;
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GTTGCTCGACGACCAACATCATCAAGAAGATCC 1414

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CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR PILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 8919
RESULT 6
US-11-099-686-8739/c
US-11-099-686-8739/c
Sequence 8739, Application US/11098686
Publication No. US20060024696A1
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS
FILE REPERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
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; ORGANISM: Lawsonia
US-11-098-686-8919
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US-11-098-686-8919
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Best Local Sim
Matches 203;
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TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
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RESULT 7
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PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8739
LENGTH: 1457619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Lawsonia intracellularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1014 TGGTGAAAAAGTGGTGATGACCAACGGTGTCTTTGACATCCTGCACGCCGGGCACGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTATCTGGCAAATGCCCGCAAGCTGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGC
                                                                                                                                                                                                                 AGAAGAGATTGCCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAA 1370
                                                                                                                                                                                                                                                         ATTACAATTAATTGAAGCTATTCAACCTAATGTACTAGTTAAAGGTGGTGATTGGTGTGT
                                                                                                                                                                                                                                                                                                                                           TTTTGTATTAGCTCATCTTGAACTTATAGATTTCATTATTGGTTTTGAAGAAGATACACC
                                                                                                                                                                                                                                                                                                                                                                                GATTGTGCTGGGCGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAGAGGACACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTTCTGACTAGAGCAAAAACATATGGAGATATTCTGGTTCTTGGATTAAATACTGATAA 21284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGGAAAAAATTATCTTTÄCAAACGGTTGTTATGATATTCTTCATCCTGGACATCTTGA 21344
                                                                                   TTTTCTTGAAGGACATTCAACAAGTGGGTTAGTACAAAAAATACGTAATAAAAAA
                                                                                                                           CTTTGAAGACGGTTGCTCGACGACCAACATCATCAAGAAGATCCAACAGGATAAA 1425
                                                                                                                                                                       AGAACAAATTATAGGTAAAGAGTTTGTAGAGCGCAATAATGGTCTTGTATTAAGTCTTCC
                                                                                                                                                                                                                                                                                                   GCAGCGCTTGATCGCCGGGATCTTGCCAGATCTGCTGGTGAAAGGCCGGCGACTATAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTGTTAAACGGTTAGGAAAAGATCCAGATAGACCATTTAATCCTTTCCATATTCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCACCAAACGGCTGAAAGGGGATTCCC---GCCCGGTAAACCCCACTCGAACAGCGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 1.4e-08;
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PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOPTWARE: PRESESEQ for Windows Version 4.0
SEQ ID NO 9716
LENGTH: 1038
TYPE: DNA
ORGANISM: Lawsonia intracellularis
US-11-098-686-9716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9716, Application US/11098686
Publication No. US20060024696A1
GENERAL INFORMATION:
APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METH
                                                                                         Query Match
Best Local Similarity
                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/11/098,686 CURRENT FILING DATE: 2005-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 09531-128001
                           37
GTGATGGTGGTGGTGGATGCTGGATGCTTACTGGTACGGCCCCACCAGTCGTATC 96
                                                                     Conservative
                                                                                         4.4%;
                                                                     0
                                                                  Score 62.4; DB 12;
Pred. No. 6.1e-09;
0; Mismatches 171;
                                                                       Indels
                                                                                                              Length
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; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-11-098-686-8739
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SEQ ID NO 8739
LENGTH: 1457619
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Best Local Similarity
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CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR PPLICATION NUMBER: US 60/416,395
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
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APPLICANT: Kapur, V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: Kapur, Vivek and Gebhart, Connie J.
ITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
ITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1014025 GTTCTTGTCGTTGGTGATATAATGTTAGATAATTTATCTTATTGGTGTTTCAGATCGTATT 1014084
  1014325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                            ACGGGCATTGACGATGCAGCGCGCGCGCTGAGTAAATCTCTGGCCGACGTCAACGTCAAA 276
                                                                                                                                                                                                                                                                                                                                                                                    gcgcctaacgtgcgatgaatatcgcttctctcggtgctaatgcacgcctggtcggttg
                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTCCTGAGGCACCTGTCCCTATTGTAÀAAATAGAGAATGAAAAGCAATCTCTTGGGGGGT 1014144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGACAACAGATGATACGACTTGATCATGAGGAAAGT
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                                                                                                                                                                                                                        GTAGGACAAGACCAAAGTGGAGAAAAAATTCAAGATCTTTTAAGTACAAGGGGAATTTTA
                                                                                                                                                                                                                                                                                                                                   GCAGGGAATGTAGCAAGGAGTATTGCTGCTCTGGGTGGAAAGGTAACGATTATTGGGGCT 1014204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGCCGGAAGCGCCGGTGCCCGTGGTTAAAGTGAATACCATCGAAGAACGTCCGGGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTCAATTATAACATTTGCAAATCGTCAAACAACAGTAAAAACACGTGTGATGGCTCAC
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                                                    AACCAACAGCTGATCCGTCTGGATTTTGAAGAAGGT
                                                                                                             TCTTCAATTATAACATTTGCAAATCGTCAAACAACAGTAAAAACACGTGTGATGGCTCAC
                                                                                                                                                            TGCGACTTCGTTTCTGTACCGACGCATCCGACCATTACCAAATTACGGGTACTTTCCCGC 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 6
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                                                      372
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; TYPE: DNA
; ORGANISM: Thermobifida fusca
US-10-858-730-141
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; ORGANISM: Lawsonia intracellularis
US-11-098-686-6509
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                                                                SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 141
LENGTH: 3477
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6509
LENGTH: 200
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/11/098,686 CURRENT FILING DATE: 2005-04-04 PRIOR APPLICATION NUMBER: PCT/US03/31318 PRIOR FILING DATE: 2003-10-01 PRIOR APPLICATION NUMBER: US 60/416,395 PRIOR FILING DATE: 2002-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND MET
                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                     PRIOR FILING DATE: 2004-03-10
                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/858,730
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/475,000
PRIOR FILING DATE: 2003-05-30
                                                                                                                                                                                                                                                                                            APPLICANT: YOTGEY, PETET S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: 14184-030001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 09531-128001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bailey, Richard B.
APPLICANT: Blomquist, Paul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 TCGCCGGAAGCGCCGGTGCCCGTGGTTAAAGTGAATACCATCGAAGAACGTCCGGGCCGGC 156
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O'Toole, George
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Madden, Kevin T.
                                                                                                                                                                                                                                                                                                                                                                                  Trueheart, Joshua
Walbridge, Michael J.
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58.2%;
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Pred. No. 9.3e-07;
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GRGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1140)
OTHER INFORMATION: Ceres Seq. ID
US-11-096-568A-31210
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US-11-096-568A-31210
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APPLICANT: Alexandrov, Nickolai et al.
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TILE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT PLLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 31210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 144; Conserv
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                                                                                                                                                                                                                                                                                              Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                              ocal Similarity
 1042
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                                  859
                                                                       982
                                                                                                                                                                                                                                                          679 GCTCTGTTAGTGACCCGTTCCGAACAGGGTATGTCGCTGCTGCAACCGGGTAAAGCGCCG 738
                                                                                                                                                                               739 CTGCATATGCCAACCCAAGCGCAGGAAGTGTATGACGTTACCGGTGCGGGCGACACGGTG 798
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                                                                                                         ATTGGCGTCCTGGCAACGCTGGCAGCGGTAATTCGCTGGAAGAAGCCTGCTTCTTT 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGGGCGCCCTCATGGCGCTGACCATCGACGAGCAGGGGGCAGGCGCGGACCGCGAACG
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 GCTGCTGCAGCTGC 1055
                                    GCCAATGCGGCGGC 872
                                                                       ACTGCAGCATTTGCAGTCGCTATGGTAGAGGGCAAGTCCCATGAGGAATGCTTGAGATTT
                                                                                                                                              CAGCAGTCTATCATACCGGCTGCACAAGTGGTTGATACTACAGGAGCTGGGGATACTTTC
                                                                                                                                                                                                                       GTTCTAGTAAAACTCGGGTCCAAAGGATCTGCACTATTCATACAAGGGGAAAAAACCAATC 921
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49.5%;
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Pred. No. 0.0082;
                                                                                                                                                                                                                                                                                                              Score 37.2; DB 9;
Pred. No. 0.41;
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CURRENT APPLICATION NUMBER: US/11/205,109
CURRENT FILING DATE: 2005-08-17
PRIOR APPLICATION NUMBER: US/09/976,059
PRIOR FILING DATE: 2001-10-15
PRIOR FILING DATE: 2001-10-15
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 46
SOPTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 88421
TYPE: DNA
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US-11-205-109-1
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments
TITLE OF INVENTION: Therby
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/11205109
Publication No. US20050287641A1
GENERAL INFORMATION:
APPLICANT: Farnet, Chris
APPLICANT: Zazgoulos, Emmanuel
Applicant
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CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 31087
LENGTH: 2253
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
FILE REFERENCE: 3002-20S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 2750-1592PUS2
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NAME/KEY: misc_feature
LOCATION: (1)..(2253)
OTHER INFORMATION: Ceres Seq. ID no. 4987027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                         NAMB/KEY: misc_feature
LOCATION: (2077)..(3078)
OTHER INFORMATION: ORF 1; positive strandedness
NAME/KEY: misc_feature
LOCATION: (3118)..(4032)
OTHER INFORMATION: ORF 2
                                                                                                                                         FEATURE:
                                                                                                                                                       ORGANISM: Actinoplanes
                                                             FEATURE:
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positive

strandedness

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NAME/KEY: misc feature
LOCATION: (70659)..(71906)
OTHER INFORMATION: ORF 19;
                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (70099)..(70662)
OTHER INFORMATION: ORF 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (4038)...(5048)
OTHER INFORMATION: ORF 3;
                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (67384)..(70059)
DITHER INFORMATION: ORF 17;
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LOCATION: (66546)..(67370)
DTHER_INFORMATION: ORF 16;
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LOCATION: (12751)...(10829)
DTHER_INFORMATION: ORF 8;
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LOCATION: (9691)..(10761)
THER INFORMATION: ORF 7; positive
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LOCATION: (7703)..(6693)
OTHER INFORMATION: ORF 5;
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OTHER INFORMATION: ORF 4;
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.OCATION: (65826)..(66530)
JTHER INFORMATION: ORF 15;
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OCATION: (39713)..(65800)
WHER_INFORMATION: ORF 14;
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THER INFORMATION: ORF 11;
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OCATION: (13617)..(12802)
THER INFORMATION: ORF 9;
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.OCATION: (9464)..(8130)

YTHER INFORMATION: ORF 6;
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OCATION: (15880)..(19035)
THER INFORMATION: ORF 12;
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DCATION: (19032)..(39713)
THER INFORMATION: ORF 13,
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OCATION: (15203)..(13614)
THER INFORMATION: ORF 10;
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'ION: (15591)..(15
ON: (73439)..(71964)
INFORMATION: ORF 20;
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; LCCATION: (87454)..(88420)
; OTHER INFORMATION: ORF 33;
US-11-205-109-1
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LOCATION: (87372)..(868
OTHER INFORMATION: ORF
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LOCATION: (85556)..(86845)
OTHER INFORMATION: ORF 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (84481)..(85548)
OTHER INFORMATION: ORF 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (82587)..(84446)
OTHER INFORMATION: ORF 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (82346)..(82062)
OTHER_INFORMATION: ORF 28;
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LOCATION: (79864)..(78107)
OTHER INFORMATION: ORF 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (78110)..(76449)
OTHER_INFORMATION: ORF 24; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (75424)..(74213)
OTHER INFORMATION: ORF 22;
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LOCATION: (74216)..(73563)
OTHER INFORMATION: ORF 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (81909)..(81682)
OTHER INFORMATION: ORF 27;
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LOCATION: (81624)..(798
OTHER INFORMATION: ORF
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LOCATION: (75535)..(76464)
OTHER_INFORMATION: ORF 23;
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                                                                      63612
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                                                                                                           221
                                                                                                                                                                                                                                                        101
                                                                                                                                                                                                                                                                                            178;
                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                               CGGAAGCGCCGGTGCCCGTGGTTAAAGTGAATACCATCGAAGAACGTCCGGGCGGCGCGCG
                                ACTTCGTTTCTGTACCGACGCATCCGACCATTACCAAATTACGGGTACTTTCCCCGCAACC 340
                                                                                                         GCATTGACGATGCAGCGCGCGCGCTGAGTAAATCTCTGGCCGACGTCAACGTCAAATGCG
                                                                                                                                                                               CTAACGTGGCGATGAATATCGCTTCTCTCGGTGCTAATGCACGCCTGGTCGGGTTGACGG
                                                                                                                                                                                                                    CGGTCGCGGTGGTGGGGGTGTGTCGTGGTCCTATCGCGAGCTTGACCGTCGCTCGG
                                                                        CCCTCGAACGGTCCGCCGACGTGCTGACCGCGTTTCTCGCCGTCGCGAAGGCCGGCGGTG
                                                                                                                                                                                                                                                                                            Conservative
NCCGGTGGACTTGTCCTGGCCGCAGACGCGTATCGATGCGGTGATCGCGGACA 63731
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (86803)
ORF 32;
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                                                                                                                                                                                                                                                                                                                                                                                    positive strandedness; N-terminus
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Pred. No. 2;
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220 63611

63551

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; NUMBER OF SEQ ID NOS: 9218; SOFTWARE: SeqWin99, version 1.04; SEQ ID NO 7053; LENGTH: 699; TYPE: DNA; ORGANISM: Neisseria gonorrhoeae US-10-467-657-7053
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US-10-467-657-7053
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                                                                                                                                                                                                                                                         RESULT 15
US-10-467-657-7841
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                                                                                                                                                                                             Sequence 7841, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
                                                                         APPLICANT: CHIRON SPA
APPLICANT: FONTANA MARÍA RÍTA
APPLICANT: FIZZA MARÍAGYRAZÍA
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
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APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
APPLICANT: MONACI Elisabetta
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CURRENT FILING DATE: 2003-08-11
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                                                           FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                           1241 AGGAÇACGCCGCAGCGCTTGATCGCCGGGATCTTGCCAGATCTGCTG 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1181 AACAGCGTATGATTGTGCTGGGCGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAG 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1061 CCGGCCACGTCTCTTATCTGGCAAATGCCCGCAAGCTGGGTGACCGCTTGATTGTTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTATGTCCCGACCACGCCCAACCCGACCGGCGGTTACTATTATTATGGTAAAGAAAAGCG
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; NUMBER OF SEQ ID NOS: 9218; SOFTWARE: SeqWin99, version 1.04; SEQ ID NO 7841; SEQ ID NO 7841; LENGTH: 3513; TYPE: DNA; ORGANISM: Neisseria gonorrhoeae US-10-467-657-7841
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Best Local Similarity
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                                                                       1768
                                                                                                                                           1708
                                                                                                                                                                                                                 1648 ACGGTCAGCTTTGCCGATGCCGCGCTTGCCCAAGAAGCGGTTGGTGCAGCCGTTGCCGCG
                                                                                                                                                                                                                                                                                         1588 CGCGATGTCGGCGAAGCGCAACCGATTAAAAACCCTGCCGACCACGGCGATGTTGTCGGT 1647
                                                                                                                                                                               673
                                   793
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                                                                                                                                                                                                                                                                                                                         553 CGCTACCGCGGCGCTACGCTGTTAACGCCGAATCTCTCGGAATTTGAAGCTGTTGTCGGT
                                                                                                     GCGCCGCTGCATATGCCCAACCCCAAGCGCAGGAAGTGTATGACGTTACCGGTGCGGGCGAC 792
                                                                                                                                                                               CTCTCGGCTCTGTTAGTGACCCGTTCCGAACAGGGTATGTCGCTGCTGCAACCGGGTAAA 732
                                ACGGTGATTGGCGTCCTGGCGGCAACGCTGGCAGCGGGTAATT 835
                                                                       GACCTGCTCGAACAGCACACCCCCGCGCTGATGATGCTTGCCGTGCGCGAAGCGGGCAAA 1827
                                                                                                                                         AAATGTAAGACCGAAGAAGAGTTGTTGAGCGCGGCATGAAACTGATTGCCGATTACGAA 672
ACGCTGAACAACGCCATTGCCGAAGTGCGCGAAGCCGTCGATT 1870
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45.6%;
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Search co completed: March 18, ne : 554 secs 2006, 20:19:09